

GTTTAGTCTGCAGCCGAGCAGCTAAAGGAGAGAAATCGCTCAGGAAAGACACACTGCAGACTCCACCGCACCCCTGC																			79	
AATAGATGGTTCCGACTACACAAGGAGAGAAACCGGAGGTGACACTCTCTGCCTGGAAGAGGACGAAACGACCCAAA																			158	
CAAACGCAAGGACTGGACTCCATGCCGAAAGGTATCTGGAAGTCGTGACACCGTGTGTATATAAACAACAAAGTTTTCGGAGCT																			237	
GTTAATTGCTGTGCTGTATTATTAAGAGACGCTTTCAAGTTTCAAGTACCAATGTAGCTTTACGTTGCCAAAGGAAGT																			316	
TGAGGCAATTGCTTTTGCTGTTTTAACTTGCTCTGTGAGGGAATCTCATAAACTGACCA																			5	
M H Q M N																			390	
ATG CAC CAA ATG AAT																				
A	K	M	H	F	R	F	V	A	L	L	I	V	S	F	N	H	D	V	25	
GCT	AAA	ATG	CAC	TTT	AGG	TTT	GTT	TTT	GCA	CTT	CTG	ATA	GTA	TCT	TTC	AAC	CAC	GAT	GTA	450
L	G	K	N	L	K	Y	R	I	Y	E	E	Q	R	V	G	S	V	I	A	45
CTG	GGC	AAG	AAT	TTG	AAA	TAC	AGG	ATT	TAT	GAG	GAA	CAG	AGG	GTT	GGA	TCA	GTA	ATT	GCA	510
R	L	S	E	D	V	A	D	V	L	L	L	K	L	P	N	P	S	T	V	65
AGA	CTA	TCA	GAG	GAT	GTG	GCT	GAT	GTT	TTA	TTG	AAG	CTT	CCT	AAT	CCT	TCT	ACT	GTT	CGA	570
F	R	A	M	Q	R	G	N	S	P	L	L	V	V	N	E	D	N	G	E	85
TTT	CGA	GCC	ATG	CAG	AGG	GGA	AAT	TCT	CCT	CTA	CTT	GTA	GTA	AAC	GAG	GAT	AAT	GGG	GAA	630

Fig. 1A

I	S	I	G	A	T	I	D	R	E	Q	L	C	Q	K	N	L	N	C	S	105
ATC	AGC	ATA	GGG	GCT	ACA	ATT	GAC	CGT	GAA	CAA	CTG	TGC	CAG	AAA	AAC	TTG	AAC	TGT	TCC	690
I	E	F	D	V	I	T	L	P	T	E	H	L	Q	L	F	H	I	E	V	125
ATA	GAG	TTT	GAT	GTG	ATC	ACT	CTA	CCC	ACA	GAG	CAT	CTG	CAG	CTT	TTC	CAT	ATT	GAA	GTT	750
E	V	L	D	I	N	D	N	S	P	Q	F	S	R	S	L	I	P	I	E	145
GAA	GTG	CTG	GAT	ATT	AAT	GAC	AAT	TCT	CCC	CAG	TTT	TCA	AGA	TCT	CTC	ATA	CCT	ATT	GAG	810
I	S	E	S	A	A	V	G	T	R	I	P	L	D	S	A	F	D	P	D	165
ATA	TCT	GAG	AGT	GCA	GCA	GTT	GGG	ACT	CGC	ATT	CCC	CTG	GAC	AGT	GCA	TTT	GAT	CCA	GAT	870
V	G	E	N	S	L	H	T	Y	S	L	S	A	N	D	F	F	N	I	E	185
GTT	GGG	GAA	AAT	TCC	CTC	CAC	ACA	TAC	TCG	CTC	TCT	GCC	AAT	GAT	TTT	TTT	AAT	ATC	GAG	2/361 930
V	R	T	R	T	D	G	A	K	Y	A	E	L	I	V	V	R	E	L	D	205
GTT	CGG	ACC	AGG	ACT	GAT	GGA	GCC	AAG	TAT	GCA	GAA	CTC	ATA	GTG	GTC	AGA	GAG	TTA	GAT	990
R	E	L	K	S	S	Y	E	L	Q	L	T	A	S	D	M	G	V	P	Q	225
CGG	GAG	CTG	AAG	TCA	AGC	TAC	GAG	CTT	CAG	CTC	ACT	GCC	TCA	GAC	ATG	GGA	GTA	CCT	CAG	1050
R	S	G	S	S	I	L	K	I	S	I	S	D	S	N	D	N	S	P	A	245
AGG	TCT	GGC	TCA	TCC	ATA	CTA	AAA	ATA	AGC	ATT	TCA	GAC	TCC	AAT	GAC	AAC	AGC	CCT	GCT	1110

Fig. 1B

F E Q Q S Y I I Q L L E N S P V G T L L 265
 TTT GAG CAG CAA TCT TAT ATA ATA CAA CTC TTA GAA AAC TCC CCG GTT GGC ACT TTG CTC 1170

L D L N A T D P D E G A N G K I V Y S F 285
 TTA GAT CTG AAT GCC ACG GAT CCA GAT GAG GGC GCT AAT GGG AAA ATT GTA TAT TCC TTC 1230

S S H V S P K I M E T F K I D S E R G H 305
 AGC AGT CAT GTG TCT CCC AAA ATT ATG GAG ACT TTT AAA ATT GAT TCT GAA AGA GGA CAT 1290

L T L F K Q V D Y E I T K S Y E I D V Q 325
 TTG ACT CTT TTC AAG CAA GTG GAT TAT GAA ATC ACC AAA TCC TAT GAG ATT GAT GTT CAG 1350

A Q D L G P N S I P A H C K I I I K V V 345
 GCT CAA GAT TTG GGT CCA AAT TCA ATC CCA GCC CAT TGC AAA ATT ATA ATT AAG GTT GTG 1410

D V N D N K P E I N I N L M S P G K E E 365
 GAT GTT AAT GAC AAT AAA CCT GAA ATT AAC ATC AAC CTC ATG TCC CCT GGA AAA GAA GAA 1470

I S Y I F E G D P I D T F V A L V R V Q 385
 ATA TCT TAT ATT TTT GAA GGG GAT CCT ATT GAT ACA TTT GTT GCT TTG GTC AGA GTT CAG 1530

D K D S G L N G E I V C K L H G H G H F 405
 GAC AAG GAT TCT GGG CTG AAT GGA GAA ATA GTT TGT AAG CTT CAT GGA CAT GGT CAC TTT 1590

Fig. 1C

K L Q K T Y E N N Y L I L T N A T L D R 425
 AAA CTT CAG AAG ACA TAT GAA AAC AAT TAT TTA ATC TTA ACT AAT GCC ACA CTG GAT AGA 1650

 E K R S E Y S L T V I A E D R G T P S L 445
 GAA AAG AGA TCT GAG TAT AGT TTG ACT GTA ATC GCT GAG GAC AGG GGG ACA CCC AGT CTC 1710

 S T V K H F T V Q I N D I N D N P P H F 465
 TCT ACA GTG AAA CAT TTT ACA GTT CAA ATC AAT GAT ATC AAT GAC AAT CCA CCC CAC TTC 1770

 Q R S R Y E F V I S E N N S P G A Y I T 485
 CAG AGA AGC CGA TAT GAA TTT GTA ATT TCA GAA AAT AAC TCA CCA GGG GCA TAT ATC ACC 1830

 T V T A T D P D L G E N G Q V T Y T I L 505
 ACT GTT ACA GCC ACA GAT CCT GAT CTT GGA GAA AAT GGG CAA GTG ACA TAC ACC ATC TTG 1890

 E S F I L G S S I T T Y V T I D P S N G 525
 GAG AGT TTT ATT CTA GGA AGT TCC ATA ACT ACA TAT GTA ACC ATT GAC CCA TCT AAT GGA 1950

 A I Y A L R I F D H E E V S Q I T F V V 545
 GCC ATC TAT GCC CTC AGA ATC TTT GAT CAT GAA GAA GTG AGT CAG ATC ACT ACT TTT GTG GTA 2010

 E A R D G G S P K Q L V S N T T V V L T 565
 GAA GCA AGA GAT GGA AGC AGC CCG AAG CAA CTG GTA AGC AAT ACC ACA GTT GTG CTC ACC 2070

Fig. 1D

I I D E N D N V P V V I G P A L R N N T 585
ATC ATT GAC GAA AAT GAC AAC GTT CCT GTG GTT ATA GGG CCT GCA TTG CGT AAT AAT ACG 2130

A E I T I P K G A E S G F H V T R I R A 605
GCA GAA ATC ACC ATT CCC AAA GGG GCT GAA AGT GGC TTT CAT GTC ACA AGA ATA AGG GCA 2190

I D R D S G V N A E L S C A I V A G N E 625
ATT GAC AGA GAC TCT GGT GTG AAT GCT GAA CTC AGC TGC GCC ATA GTA GCA GGT AAT GAG 2250

E N I F I I D P R S C D I H T N V S M D 645
GAG AAT ATC TTC ATA ATT GAT CCA CGA TCA TGT GAC ATC CAT ACC AAC GTT AGC ATG GAT 2310

S V P Y T E W E L S V I I Q D K G N P Q 665
TCT GTT CCC TAC ACA GAA TGG GAG CTG TCA GTT ATC ATT CAG GAC AAA GGC AAT CCT CAG 2370

L H T K V L L K C M I F E Y A E S V T S 685
CTA CAT ACC AAA GTC CTT CTG AAG TGC ATG ATC TTT GAA TAT GCA GAG TCG GTG ACA AGT 2430

T A M T S V S Q A S L D V S M I I I I S 705
ACA GCA ATG ACT TCA GTA AGC CAG GCA TCC TTG GAT GTC TCC ATG ATA ATA ATT ATT TCC 2490

L G A I C A V L L V I M V L F A T R C N 725
TTA GGA GCA ATT TGT GCA GTG TTG CTG GTT ATT ATG GTG CTA TTT GCA ACT AGG TGT AAC 2550

Fig. 1E

R	E	K	K	D	T	R	S	Y	N	C	R	V	A	E	S	T	Y	Q	H	745
CGC	GAG	AAG	AAA	GAC	ACT	AGA	TCC	TAT	AAC	TGC	AGG	GTG	GCC	GAA	TCA	ACT	TAC	CAG	CAC	2610
H	P	K	R	P	S	R	Q	I	H	K	G	D	I	T	L	V	P	T	I	765
CAC	CCA	AAA	AGG	CCA	TCC	CGG	CAG	ATT	CAC	AAA	GGG	GAC	ATC	ACA	TTG	GTG	CCT	ACC	ATA	2670
N	G	T	L	P	I	R	S	H	H	R	S	S	P	S	S	S	P	T	L	785
AAT	GGC	ACT	CTG	CCC	ATC	AGA	TCT	CAT	CAC	AGA	TGG	TCT	CCA	TCT	TCA	TCT	CCT	ACC	TTA	2730
E	R	G	Q	M	G	S	R	Q	S	H	N	S	H	Q	S	L	N	S	L	805
GAA	AGA	GGG	CAG	ATG	GGC	AGC	CGG	CAG	AGT	CAC	AAC	AGT	CAC	CAG	TCA	CTC	AAC	AGT	TTG	2790
V	T	I	S	S	N	H	V	P	E	N	F	S	L	E	L	T	H	A	T	825
GTG	ACA	ATC	TCA	TCA	AAC	CAC	GTG	CCA	GAG	AAT	TTC	TCA	TTA	GAA	CTC	ACC	CAC	GCC	ACT	2850
P	A	V	E	Q	V	S	Q	L	L	S	M	L	H	Q	G	Q	Y	Q	P	845
CCT	GCT	GTT	GAG	CAG	GTC	TCT	CAG	CTT	CTT	TCA	ATG	CTT	CAC	CAG	GGG	CAA	TAT	CAG	CCA	2910
R	P	S	F	R	G	N	K	Y	S	R	S	Y	R	Y	A	L	Q	D	M	865
AGA	CCA	AGT	TTT	CGA	GGA	AAC	AAA	TAT	TCC	AGG	AGC	TAC	AGA	TAT	GCC	CTT	CAA	GAC	ATG	2970
D	K	F	S	L	K	D	S	G	R	G	D	S	E	A	G	D	S	D	Y	885
GAC	AAA	TTT	AGC	TTG	AAA	GAC	AGT	GGC	CGT	GGT	GAC	AGT	GAG	GCA	GGA	GAC	AGT	GAT	TAT	3030

Fig. 1F

D	L	G	R	D	S	P	I	D	R	L	L	G	E	G	F	S	D	L	F	905
GAT	TTG	GGG	CGA	GAT	TCT	CCA	ATA	GAT	AGG	CTG	CTG	GGT	GAA	GGA	TTC	AGC	GAC	CTG	TTT	3090
L	T	D	G	R	I	P	A	A	M	R	L	C	T	E	E	C	R	V	L	925
CTC	ACA	GAT	GGA	AGA	ATT	CCA	GCA	GCT	ATG	AGA	CTC	TGC	ACG	GAG	GAG	TGC	AGG	GTC	CTG	3150
G	H	S	D	Q	C	W	M	P	P	L	P	S	P	S	S	D	Y	R	S	945
GGA	CAC	TCT	GAC	CAG	TGC	TGG	ATG	CCA	CCA	CTG	CCC	TCA	CCG	TCT	TCT	GAT	TAT	AGG	AGT	3210
N	M	F	I	P	G	E	E	F	P	T	Q	P	Q	Q	Q	H	P	H	Q	965
AAC	ATG	TTC	ATT	CCA	GGG	GAA	GAA	TTC	CCA	ACG	CAA	CCC	CAG	CAG	CAG	CAT	CCA	CAT	CAG	3270
S	L	E	D	D	A	Q	P	A	D	S	G	E	K	K	K	S	F	S	T	985
AGT	CTT	GAG	GAT	GAC	GCT	CAG	CCT	GCA	GAT	TCC	GGT	GAA	AAG	AAG	AAG	AGT	TTT	TCC	ACC	3330
F	G	K	D	S	P	N	D	E	D	T	G	D	T	S	T	S	S	L	L	1005
TTT	GGA	AAG	GAC	TCC	CCA	AAC	GAT	GAG	GAC	ACT	GGG	GAT	ACC	AGC	ACA	TCA	TCT	CTG	CTC	3390
S	E	M	S	S	V	F	Q	R	L	L	P	P	S	L	D	T	Y	S	E	1025
TCG	GAA	ATG	AGC	AGT	GTG	TTC	CAG	CGT	CTC	TTA	CCG	CCT	TCC	CTG	GAC	ACC	TAT	TCT	GAA	3450
C	S	E	V	D	R	S	N	S	L	E	R	R	K	G	P	L	P	A	K	1045
TGC	AGT	GAG	GTG	GAT	CGG	TCC	AAC	TCC	CTG	GAG	CGC	AGG	AAG	GGA	CCC	TTG	CCA	GCC	AAA	3510

Fig. 1G

AGACAAATGATGAAAAACAGAACTAAAGTCAATGTTTCCCTGACTCCCAGGCCCTACTATTCCAGGCCATCACACTGGCCT 4494
 GTTCCGGAGAAATATTTCTCTCACAAATATATATCTACTTATAATTAATGTTAAACAATAAAATTTTATTCCATCCTTGTGA 4573
 GTATGAAACATGCTCCAAGGAAATGGAACTGTCTCTTAAATGGATAACAGTATGTGTTCTAATGGCATAAAAATATTAC 4652
 TGGATAAAAAACAGTTGTGTCAGTGTCTCTCCCTAAGGTAGTAAATATAATTGACTTATTCTGAACCCATTCTATTTTGAA 4731
 TCTCCCCCTTTCTCACAAATACCTTGAACATTTTAAATCTTTTGGAAATATTGTCTTTCTTTGTTATAAATACTATTCATTTT 4810
 AGCTTTTGTCTCCAGTGCAATGATCTCATATTTTGTCTTTTATTTTATAGTATAAGAACATTTATAAAAAATCATATTTTGT 4889
 TACTGCAATTTGTTTATTTGTGTGGCAAAATGAGAAATCCTTTATTTATTTGTGCTGTGATCTCTCTGTGGAAATGC 4968
 CTTGGTGAGAGAGATGCTTATATGACTATTATCATTTCTGACCAAGCTTCTAATTAATGTTATTCTAATAATACACTA 5047
 TCTTGATTGTACTCTCCAGAAAAATTTTCTGTGAGTGAATAAAGAAAAATTAAGTAAAAAATAAAAAA 5121

Fig. 11

GTTTAGTCTGCAGCCGAGCAGCTAAAGGAGAAAGAAATCGCTCAGGAAAGACACACTGCAGACTCCACCGCACCCCTGC	79
AATAGATGGGTCCGACTACACAAGGAGAAACCGGAGGTGACACTCTCTGCCCTGGAAAGAGGACGAAACGACCAAA	158
CAACGCAAGGACTGGACTCCATGCCGAAGGTATCTGAAAGTCGTGACACGGTGTGTATAAAACAAAAGTTTGGCAGCT	237
GTTAAATTGCTGTGCTGTATTATTAAAGAGACGCTTTCAAGTTTCAAGTACCAAAATGTAGCTTTACGTTGCCAAAAGGAAGT	316
TGAGGCAATTGCTTTTGCTGTGCTTTTAACTTGCTCTGTGAGGAAATCTCATAAACTGACCA ATG CAC CAA ATG AAT	5 390
A K M H F R F V F A L L I V S F N H D V	25
GCT AAA ATG CAC TTT AGG TTT GTT TTT GCA CTT CTG ATA GTA TCT TTC AAC CAC GAT GTA	450
L G K N L K Y R I Y E E Q R V G S V I A	45
CTG GGC AAG AAT TTG AAA TAC AGG ATT TAT GAG GAA CAG AGG GTT GGA TCA GTA ATT GCA	510
R L S E D V A D V L L L K L P N P S T V R	65
AGA CTA TCA GAG GAT GTG GCT GAT GTT TTA TTG AAG CTT CCT AAT CCT TCT ACT GTT CGA	570
F R A M Q R G N S P L L V V N E D N G E	85
TTT CGA GCC ATG CAG AGG GGA AAT TCT CCT CTA CTT GTA GTA AAC GAG GAT AAT GGG GAA	630
I S I G A T I D R E Q L C Q K N L N C S	105
ATC AGC ATA GGG GCT ACA ATT GAC CGT GAA CAA CTG TGC CAG AAA AAC TTG AAC TGT TCC	690

Fig. 2A

I	E	F	D	V	I	T	L	P	T	E	H	L	Q	L	F	H	I	E	V	125
ATA	GAG	TTT	GAT	GTG	ATC	ACT	CTA	CCC	ACA	GAG	CAT	CTG	CAG	CTT	TTC	CAT	ATT	GAA	GTT	750
E	V	L	D	I	N	D	N	S	P	Q	F	S	R	S	L	I	P	I	E	145
GAA	GTG	CTG	GAT	ATT	AAT	GAC	AAT	TCT	CCC	CAG	TTT	TCA	AGA	TCT	CTC	ATA	CCT	ATT	GAG	810
I	S	E	S	A	A	V	G	T	R	I	P	L	D	S	A	F	D	P	D	165
ATA	TCT	GAG	AGT	GCA	GCA	GTT	GGG	ACT	CGC	ATT	CCC	CTG	GAC	AGT	GCA	TTT	GAT	CCA	GAT	870
V	G	E	N	S	L	H	T	Y	S	L	S	A	N	D	F	F	N	I	E	185
GTT	GGG	GAA	AAT	TCC	CTC	CAC	ACA	TAC	TCG	CTC	TCT	GCC	AAT	GAT	TTT	TTT	AAT	ATC	GAG	930
V	R	T	R	T	D	G	A	K	Y	A	E	L	I	V	V	R	E	L	D	205
GTT	CGG	ACC	AGG	ACT	GAT	GGA	GCC	AAG	TAT	GCA	GAA	CTC	ATA	GTG	GTC	AGA	GAG	TTA	GAT	990
R	E	L	K	S	S	Y	E	L	Q	L	T	A	S	D	M	G	V	P	Q	225
CGG	GAG	CTG	AAG	TCA	AGC	TAC	GAG	CTT	CAG	CTC	ACT	GCC	TCA	GAC	ATG	GGA	GTA	CCT	CAG	1050
R	S	G	S	S	I	L	K	I	S	I	S	D	S	N	D	N	S	P	A	245
AGG	TCT	GGC	TCA	TCC	ATA	CTA	AAA	ATA	AGC	ATT	TCA	GAC	TCC	AAT	GAC	AAC	AGC	CCT	GCT	1110
F	E	Q	Q	S	Y	I	I	Q	L	L	E	N	S	P	V	G	T	L	L	265
TTT	GAG	CAG	CAA	TCT	TAT	ATA	ATA	CAA	CTC	TTA	GAA	AAC	TCC	CCG	GTT	GGC	ACT	TTG	CTC	1170

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Fig. 2B

L D L N A T D P D E G A N G K I V Y S F 285
 TTA GAT CTG AAT GCC ACG GAT CCA GAT GAG GGC GCT AAT GGG AAA ATT GTA TAT TCC TTC 1230

 S S H V S P K I M E T F K I D S E R G H 305
 AGC AGT CAT GTG TCT CCC AAA ATT ATG GAG ACT TTT AAA ATT GAT TCT GAA AGA GGA CAT 1290

 L T L F K Q V D Y E I T K S Y E I D V Q 325
 TTG ACT CTT TTC AAG CAA GTG GAT TAT GAA ATC ACC AAA TCC TAT GAG ATT GAT GTT CAG 1350

 A Q D L G P N S I P A H C K I I I K V V 345
 GCT CAA GAT TTG GGT CCA AAT TCA ATC CCA GCC CAT TGC AAA ATT ATA ATT AAG GTT GTG 1410

 D V N D N K P E I N I N L M S P G K E E 365
 GAT GTT AAT GAC AAT AAA CCT GAA ATT AAC ATC AAC CTC ATG TCC CCT GGA AAA GAA GAA 1470

 I S Y I F E G D P I D T F V A L V R V Q 385
 ATA TCT TAT ATT TTT GAA GGG GAT CCT ATT GAT ACA TTT GTT GCT TTG GTC AGA GTT CAG 1530

 D K D S G L N G E I V C K L H G H F 405
 GAC AAG GAT TCT GGG CTG AAT GGA GAA ATA GTT TGT AAG CTT CAT GGA CAT GGT CAC TTT 1590

 K L Q K T Y E N N Y L I L T N A T L D R 425
 AAA CTT CAG AAG ACA TAT GAA AAC AAT TAT TTA ATC TTA ACT AAT GCC ACA CTG GAT AGA 1650

Fig. 2C

E	K	R	S	E	Y	S	L	T	V	I	A	E	D	R	G	T	P	S	L	445
GAA	AAG	AGA	TCT	GAG	TAT	AGT	TTG	ACT	GTA	ATC	GCT	GAG	GAC	AGG	GGG	ACA	CCC	AGT	CTC	1710
S	T	V	K	H	F	T	V	Q	I	N	D	I	N	D	N	P	P	H	F	465
TCT	ACA	GTG	AAA	CAT	TTT	ACA	GTT	CAA	ATC	AAT	GAT	ATC	AAT	GAC	AAT	CCA	CCC	CAC	TTC	1770
Q	R	S	R	Y	E	F	V	I	S	E	N	N	S	P	G	A	Y	I	T	485
CAG	AGA	AGC	CGA	TAT	GAA	TTT	GTA	ATT	TCA	GAA	AAT	AAC	TCA	CCA	GGG	GCA	TAT	ATC	ACC	1830
T	V	T	A	T	D	P	D	L	G	E	N	G	Q	V	T	Y	T	I	L	505
ACT	GTT	ACA	GCC	ACA	GAT	CCT	GAT	CTT	GGA	GAA	AAT	GGG	CAA	GTG	ACA	TAC	ACC	ATC	TTG	1890
E	S	F	I	L	G	S	S	I	T	T	Y	V	T	I	D	P	S	N	G	525
GAG	AGT	TTT	ATT	CTA	GGA	AGT	TCC	ATA	ACT	ACA	TAT	GTA	ACC	ATT	GAC	CCA	TCT	AAT	GGA	1950
A	I	Y	A	L	R	I	F	D	H	E	E	V	S	Q	I	T	F	V	V	545
GCC	ATC	TAT	GCC	CTC	AGA	ATC	TTT	GAT	CAT	GAA	GAA	GTG	AGT	CAG	ATC	ACT	TTT	GTG	GTA	2010
E	A	R	D	G	G	S	P	K	Q	L	V	S	N	T	T	V	V	L	T	565
GAA	GCA	AGA	GAT	GGA	GGA	AGC	CCG	AAG	CAA	CTG	GTA	AGC	AAT	ACC	ACA	GTT	GTG	CTC	ACC	2070
I	I	D	E	N	D	N	V	P	V	V	I	G	P	A	L	R	N	N	T	585
ATC	ATT	GAC	GAA	AAT	GAC	AAC	GTT	CCT	GTG	GTT	ATA	GGG	CCT	GCA	TTG	CGT	AAT	AAT	ACG	2130

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Fig. 2D

A E I T I P K G A E S G F H V T R I R A 605
 GCA GAA ATC ACC ATT CCC AAA GGG GCT GAA AGT GGC TTT CAT GTC ACA AGA ATA AGG GCA 2190

 I D R D S G V N A E L S C A I V A G N E 625
 ATT GAC AGA GAC TCT GGT GTG AAT GCT GAA CTC AGC TGC GCC ATA GTA GCA GGT AAT GAG 2250

 E N I F I I D P R S C D I H T N V S M D 645
 GAG AAT ATC TTC ATA ATT GAT CCA CGA TCA TGT GAC ATC CAT ACC AAC GTT AGC ATG GAT 2310

 S V P Y T E W E L S V I I Q D K G N P Q 665
 TCT GTT CCC TAC ACA GAA TGG GAG CTG TCA GTT ATC ATT CAG GAC AAA GGC AAT CCT CAG 2370

 L H T K V L L K C M I F E Y A E S V T S 685
 CTA CAT ACC AAA GTC CTT CTG AAG TGC ATG ATC TTT GAA TAT GCA GAG TCG GTG ACA AGT 2430

 T A M T S V S Q A S L D V S M I I I I S 705
 ACA GCA ATG ACT TCA GTA AGC CAG GCA TCC TTG GAT GTC TCC ATG ATA ATA ATT ATT TCC 2490

 L G A I C A V L L V I M V L F A T R C N 725
 TTA GGA GCA ATT TGT GCA GTG TTG CTG GTT ATT ATG GTG CTA TTT GCA ACT AGG TGT AAC 2550

 R E K K D T R S Y N C R V A E S T Y Q H 745
 CGC GAG AAG AAA GAC ACT AGA TCC TAT AAC TGC AGG GTG GCC GAA TCA ACT TAC CAG CAC 2610

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Fig. 2E

H	P	K	R	P	S	R	Q	I	H	K	G	D	I	T	L	V	P	T	I	765
CAC	CCA	AAA	AGG	CCA	TCC	CGG	CAG	ATT	CAC	AAA	GGG	GAC	ATC	ACA	TTG	GTG	CCT	ACC	ATA	2670
N	G	T	L	P	I	R	S	H	H	R	S	S	P	S	S	S	P	T	L	785
AAT	GGC	ACT	CTG	CCC	ATC	AGA	TCT	CAT	CAC	AGA	TCG	TCT	CCA	TCT	TCA	TCT	CCT	ACC	TTA	2730
E	R	G	Q	M	G	S	R	Q	S	H	N	S	H	Q	S	L	N	S	L	805
GAA	AGA	GGG	CAG	ATG	GGC	AGC	CGG	CAG	AGT	CAC	AAC	AGT	CAC	CAG	TCA	CTC	AAC	AGT	TTG	2790
V	T	I	S	S	N	H	V	P	E	N	F	S	L	E	L	T	H	A	T	825
GTG	ACA	ATC	TCA	TCA	AAC	CAC	GTG	CCA	GAG	AAT	TTC	TCA	TTA	GAA	CTC	ACC	CAC	GCC	ACT	2850
P	A	V	E	V	S	Q	L	L	S	M	L	H	Q	G	Q	Y	Q	P		844
CCT	GCT	GTT	GAG	GTC	TCT	CAG	CTT	CTT	TCA	ATG	CTT	CAC	CAG	GGG	CAA	TAT	CAG	CCA		2907
R	P	S	F	R	G	N	K	Y	S	R	S	Y	R	Y	A	L	Q	D	M	864
AGA	CCA	AGT	TTT	CGA	GGA	AAC	AAA	TAT	TCC	AGG	AGC	TAC	AGA	TAT	GCC	CTT	CAA	GAC	ATG	2967
D	K	F	S	L	K	D	S	G	R	G	D	S	E	A	G	D	S	D	Y	884
GAC	AAA	TTT	AGC	TTG	AAA	GAC	AGT	GGC	CGT	GGT	GAC	AGT	GAG	GCA	GGA	GAC	AGT	GAT	TAT	3027
D	L	G	R	D	S	P	I	D	R	L	L	G	E	G	F	S	D	L	F	904
GAT	TTG	GGG	CGA	GAT	TCT	CCA	ATA	GAT	AGG	CTG	CTG	GGT	GAA	GGA	TTC	AGC	GAC	CTG	TTT	3087

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Fig. 2F

L T D G R I P A A M R L C T E E C R V L 924
 CTC ACA GAT GGA AGA ATT CCA GCA GCT ATG AGA CTC TGC ACG GAG GAG TGC AGG GTC CTG 3147

G H S D Q C W M P P L P S P S D Y R S 944
 GGA CAC TCT GAC CAG TGC TGG ATG CCA CCA CTG CCC TCA CCG TCT TCT GAT TAT AGG AGT 3207

N M F I P G E E F P T Q P Q Q H P H Q 964
 AAC ATG TTC ATT CCA GGG GAA GAA TTC CCA ACG CAA CCC CAG CAG CAG CAT CCA CAT CAG 3267

S L E D D A Q P A D S G E K K K S F S T 984
 AGT CTT GAG GAT GAC GCT CAG CCT GCA GAT TCC GGT GAA AAG AAG AGT TTT TCC ACC 3327

F G K D S P N D E D T G D T S T S L L 1004
 TTT GGA AAG GAC TCC CCA AAC GAT GAG GAC ACT GGG GAT ACC AGC ACA TCA TCT CTG CTC 3387

S E M S S V F Q R L L P P S L D T Y S E 1024
 TCG GAA ATG AGC AGT GTG TTC CAG CGT CTC TTA CCG CCT TCC CTG GAC ACC TAT TCT GAA 3447

C S E V D R S N S L E R R K G P L P A K 1044
 TGC AGT GAG GTG GAT CGG TCC AAC TCC CTG GAG CGC AGG AAG GGA CCC TTG CCA GCC AAA 3507

T V G Y P Q G V A A W A A S T H F Q N P 1064
 ACT GTG GGT TAC CCA CAG GGG GTA GCG GCA TGG GCA GCC AGT ACG CAT TTT CAA AAT CCC 3567

Fig. 2G

T	T	N	C	G	P	P	L	G	T	H	S	S	V	Q	P	S	S	K	W	1084					
ACC	ACC	AAC	TGT	GGG	CCG	CCA	CTT	GGA	ACT	CAC	TCC	AGT	GTG	CAG	CCT	TCT	TCA	AAA	TGG	3627					
L	P	A	M	E	E	I	P	E	N	Y	E	E	D	D	F	D	N	V	L	1104					
CTG	CCA	GCC	ATG	GAG	GAG	ATC	CCT	GAA	AAT	TAT	GAG	GAA	GAT	GAT	TTT	GAC	AAT	GTG	CTC	3687					
N	H	L	N	D	G	K	H	E	L	M	D	A	S	E	L	V	A	E	I	1124					
AAC	CAC	CTC	AAT	GAT	GGG	AAA	CAC	GAA	CTC	ATG	GAT	GCC	AGT	GAA	CTG	GTG	GCA	GAG	ATT	3747					
N	K	L	L	Q	D	V	R	Q	S	*										1134					
AAC	AAA	CTG	CTT	CAA	GAT	GTC	CGC	CAG	AGC	TAG										3780					
																				17/361					
GAG	ATTT	TAG	CGA	AGCA	ATTT	TGTT	TCC	ATG	TAT	TG	AAATAG	GGAACA	CAACA	CAACAAA	ACCCT	GAAA	GAA	C		3859					
TGG	CAT	TGCC	AAATAG	TTG	CAAT	TAT	CA	TAAATG	TG	CTGT	ATAT	TGA	ATAT	TAA	ATACT	GTAT	TTT	TCG	TAT	GTACA	3938				
CAAT	GCA	AGT	GTG	ATT	TTAA	CTG	ATTT	TAAAAA	TACAT	TTG	TACCT	TATAT	TTAT	GTG	TAAAT	TTAA	CAAA	CAAAA		4017					
TTTT	AT	TTTT	TACT	CCCAT	GAC	GAC	ATG	TTTT	TCC	TAG	TCG	TG	TAG	AAACT	AGCC	ACTG	TTCAA	ATCT	GAT	ACATA	4096				
TTCA	ACC	CAAA	AGT	GTA	AGC	ACT	GCT	TAG	ATT	TTT	TG	TGG	GAA	GAAT	TAT	TAT	GT	TAT	GAA	CAACCC	CACT	4175			
GAAG	CAT	TAT	ACAA	TTCT	TAA	TTCC	ATT	CA	TTAAG	TG	ATCC	CACT	TTTT	TTCA	ATACT	TTTT	TAG	AAAT	TAAG	AAAT	CATT	AAA	4254		
ATTG	TAA	AGCT	ATTT	TAT	TG	TTAT	TTT	CT	CTACT	TTT	CTACT	AGCC	CCA	ATAG	TTG	AACT	CTT	ATAG	AAAT	CG	AAA	AAGA	4333		
TAA	AGT	GAA	AGTT	TAT	TC	AGG	ACT	GAG	AAAT	ATCT	TGA	AGG	TTAT	TTAT	TAG	ATG	ACT	ATCT	CAAA	TG	AACT	TTTT	TAT	4412	
AGAC	AAT	GAT	GAAA	ACAG	AACT	AAAT	GTT	TCC	TG	ACT	CCC	AGG	CCCC	TACT	AT	TCC	AGG	CCAT	CAC	ACT	TGG	CCT	4491		
GT	CCG	GAG	AAAT	TTCT	CTC	ACA	ATAT	TAT	ATCT	ACT	TAT	AAAT	TAT	GTA	AAAC	AAAT	TTT	TAT	TCC	ATC	CTT	GTA	4570		
GTAT	GAA	ACAT	GTCT	CCA	AGG	AAAT	GGA	ATCT	GT	CCCT	TTAA	ATG	GAT	AA	CAG	TATG	TTCT	AAAT	GG	CAT	AAA	ATAT	TAC	4649	
TGGA	TAAA	AAAC	AGT	TGT	GT	CA	GT	CTCT	CT	CTA	AGG	TAG	TAA	ATATA	AT	TG	ACT	TAT	TCT	GAA	CCCAT	TCT	ATTT	TGAA	4728

Fig. 2H

TCTCCCCTTCCCTCACAATACTTGAACATTTTAATCTTTTGGAAATATTGTCCTTTCTTTGTTATAACTATTCAATTTT 4807
 AGCTTTTGCTCCAGTGCATGATCTCATATTTTGGCTTTTATTTTAGTATAAGAACATTTATATAAAATCATATTTTGT 4886
 TACTGCAATTGTTTATTTGTTGTTGGCAAAATGAGAAATCCCTTTATTTATTTGCTGTGATCTCTCTGTGTGGAATGC 4965
 CTTGGTGAGAGAGATGCTTATATGACTATATATCATTTCTGACCAAGCTTCTATTAATGTTATTTCTAATAATACACTA 5044
 TCTTGATTGTACTCTCCAGAAAAATTTTCTGTCAGTGAAAAATAAGAAAAATTAAGTAAAAAATAAAAAA 5118

Fig. 2I

T416	1651	GAAAAGAGATCTGAGTATAGTTTGACTGTAAATCGCTGAGGACAGGGGAC	1700
AL137471	1	...AAGAGATCTGAGTATAGTTTGACTGTAAATCGCTGAGGACAGGGGAC	47
T416	1701	ACCCAGTCTCTCTACAGTGAAACATTTTACAGTTCAAATCAATGATATCA	1750
AL137471	48	ACCCAGTCTCTCTACAGTGAAACATTTTACAGTTCAAATCAATGATATCA	97
T416	1751	ATGACAAATCCACCCCACTTCAGAGAAAGCCGATATGAATTTGTAAATTTC	1800
AL137471	98	ATGACAAATCCACCCCACTTCAGAGAAAGCCGATATGAATTTGTAAATTTC	147
T416	1801	GAAAATAACTCACAGGGGCATATATCACCACTGTGTACAGCCACAGATCC	1850
AL137471	148	GAAAATAACTCACAGGGGCATATATCACCACTGTGTACAGCCACAGATCC	197
T416	1851	TGATCTTGGAGAAAAATGGGCAAGTGACATACACCATCTTGGAGAGTTT	1900
AL137471	198	TGATCTTGGAGAAAAATGGGCAAGTGACATACACCATCTTGGAGAGTTT	247
T416	1901	TTCTAGGAAGTTCCATAACTACATATGTAAACCATTGACCCATCTAATGGA	1950
AL137471	248	TTCTAGGAAGTTCCATAACTACATATGTAAACCATTGACCCATCTAATGGA	297

FIG. 4A

T416	1951	GCCATCTATGCCCTCAGAATCTTTGATCATGAAGAAGTGAGTCAGATCAC	2000
AL137471	298	GCCATCTATGCCCTCAGAATCTTTGATCATGAAGAAGTGAGTCAGATCAC	347
T416	2001	TTTTGTGTAGAAGCAAGAGATGGAGGAAAGCCCGAAGCAACTGGTAAGCA	2050
AL137471	348	TTTTGTGTAGAAGCAAGAGATGGAGGAAAGCCCGAAGCAACTGGTAAGCA	397
T416	2051	ATACCACAGTTGTGCTCACCATCATTTGACGAAAATGACAACGTTTCCTGTG	2100
AL137471	398	ATACCACAGTTGTGCTCACCATCATTTGACGAAAATGACAACGTTTCCTGTG	447
T416	2101	GTATAGGGCCTGCATTGCGTAATAATACGGCAGAAATCACCATTCCCAA	2150
AL137471	448	GTATAGGGCCTGCATTGCGTAATAATACGGCAGAAATCACCATTCCCAA	497
T416	2151	AGGGGCTGAAAAGTGGCTTTCATGTCACAAGAAATAAGGGCAATTGACAGAG	2200
AL137471	498	AGGGGCTGAAAAGTGGCTTTCATGTCACAAGAAATAAGGGCAATTGACAGAG	547
T416	2201	ACTCTGGTGTGAATGCTGAACCTCAGCTGCGCCATAGTAGCAGGTAATGAG	2250
AL137471	548	ACTCTGGTGTGAATGCTGAACCTCAGCTGCGCCATAGTAGCAGGTAATGAG	597

FIG. 4B


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T416      2251 GAGAAATATCTTCATAAATTGATCCACGATCATGTGACATCCATAACCAACGT 2300
          |||||
AL137471  598 GAGAAATATCTTCATAAATTGATCCACGATCATGTGACATCCATAACCAACGT 647

T416      2301 TAGCATGGATTCTGTTCCTTACACAGAATGGGAGCTGTCTCAGTTATCATTC 2350
          |||||
AL137471  648 TAGCATGGATTCTGTTCCTTACACAGAATGGGAGCTGTCTCAGTTATCATTC 697

T416      2351 AGGACAAAAGGCAATCCTCAGCTACATACCAAAGTCCTTCTGAAGTGCAATG 2400
          |||||
AL137471  698 AGGACAAAAGGCAATCCTCAGCTACATACCAAAGTCCTTCTGAAGTGCAATG 747

T416      2401 ATCTTTGAATATGCAGAGTCGGTGACAAGTACAGCAATGACTTCAGTAAG 2450
          |||||
AL137471  748 ATCTTTGAATATGCAGAGTCGGTGACAAGTACAGCAATGACTTCAGTAAG 797

T416      2451 CCAGGCATCCTTGGATGCTCTCCATGATAATAATTAATTTCTTAGGAGCAA 2500
          |||||
AL137471  798 CCAGGCATCCTTGGATGCTCTCCATGATAATAATTAATTTCTTAGGAGCAA 847

T416      2501 TTTGTGCAGTGTTCCTGGTTATTATGGTGCTATTGCAACTAGGTGTAAC 2550
          |||||
AL137471  848 TTTGTGCAGTGTTCCTGGTTATTATGGTGCTATTGCAACTAGGTGTAAC 897

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FIG. 4C

T416	2551	CGCGAGAAAGAAAGACACTAGATCCTATAACTGCAGGGTGGCCGAATCAAC	2600
AL137471	898	CGCGAGAAAGAAAGACACTAGATCCTATAACTGCAGGGTGGCCGAATCAAC	947
T416	2601	TTACCAGCACCAACCCAAAAGGCCATCCCGGCAGATTCAACAAGGGGACA	2650
AL137471	948	TTACCAGCACCAACCCAAAAGGCCATCCCGGCAGATTCAACAAGGGGACA	997
T416	2651	TCACATTGGTGCTTACCATAAATGGCACTCTGCCCATCAGATCTCATCAC	2700
AL137471	998	TCACATTGGTGCTTACCATAAATGGCACTCTGCCCATCAGATCTCATCAC	1047
T416	2701	AGATCGTCTCCATCTTCATCTCCTACCTTAGAAAGAGGCAGATGGGCAG	2750
AL137471	1048	AGATCGTCTCCATCTTCATCTCCTACCTTAGAAAGAGGCAGATGGGCAG	1097
T416	2751	CCGGCAGAGTCACAACAGTCACCAGTCACCTCAACAGTTTGGTGACAATCT	2800
AL137471	1098	CCGGCAGAGTCACAACAGTCACCAGTCACCTCAACAGTTTGGTGACAATCT	1147
T416	2801	CATCAAAACCAACGTGCCAGAGAAATTCTCATTAGAACTCACCCACGCCACT	2850
AL137471	1148	CATCAAAACCAACGTGCCAGAGAAATTCTCATTAGAACTCACCCACGCCACT	1197

FIG. 4D

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T416      2851 CCTGCTGTTGAGCAGGTCCTCTCAGCTTCTTTCAATGCTTCACCAGGGGCA 2900
          |||
AL137471  1198 CCTGCTGTTGAGCAGGTCCTCTCAGCTTCTTTCAATGCTTCACCAGGGGCA 1247

T416      2901 ATATCAGCCAAAGACCAAGTTTTCGAGGAAACAAATATTCCAGGAGCTACA 2950
          |||
AL137471  1248 ATATCAGCCAAAGACCAAGTTTTCGAGGAAACAAATATTCCAGGAGCTACA 1297

T416      2951 GATATGCCCTTCAAGACATGGACAAATTTAGCTTGAAAGACAGTGGCCCGT 3000
          |||
AL137471  1298 GATATGCCCTTCAAGACATGGACAAATTTAGCTTGAAAGACAGTGGCCCGT 1347

T416      3001 GGTGACAGTGAGGCAGGAGACAGTGATTATGATTTGGGGCGAGATTCTCC 3050
          |||
AL137471  1348 GGTGACAGTGAGGCAGGAGACAGTGATTATGATTTGGGGCGAGATTCTCC 1397

T416      3051 AATAGATAGGCTGCTGGGTGAAGGATTACAGCGACCTGTTTCTCACAGATG 3100
          |||
AL137471  1398 AATAGATAGGCTGTTGGGTGAAGGATTACAGCGACCTGTTTCTCACAGATG 1447

T416      3101 GAAGAAATCCAGCAGCTATGAGACTCTGCACGGAGGAGTGCAGGGTCCTG 3150
          |||
AL137471  1448 GAAGAAATCCAGCAGCTATGAGACTCTGCACGGAGGAGTGCAGGGTCCTG 1497

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FIG. 4E

T416	3151	GGACACTCTGACCACTGCTGGATGCCACCACTGCCCTCACCCGTCTTCTGA	3200
AL137471	1498	GGACACTCTGACCACTGCTGGATGCCACCACTGCCCTCACCCGTCTTCTGA	1547
T416	3201	TTATAGGAGTAACATGTTTCATTCCAGGGGAAGAATTCCCAACGCAACCCC	3250
AL137471	1548	TTATAGGAGTAACATGTTTCATTCCAGGGGAAGAATTCCCAACGCAACCCC	1597
T416	3251	AGCAGCAGCATCCACATCAGAGTCTTGAGGATGACGCTCAGCCTGCAGAT	3300
AL137471	1598	AGCAGCAGCATCCACATCAGAGTCTTGAGGATGACGCTCAGCCTGCAGAT	1647
T416	3301	TCCGGTGAAAAGAAAGAGTTTTTCCACCTTTGGAAAGGACTCCCCAAA	3350
AL137471	1648	TCCGGTGAAAAGAAAGAGTTTTTCCACCTTTGGAAAGGACTCCCCAAA	1697
T416	3351	CGATGAGGACACTGGGGATACCAGCACATCATCTCTGCTCTCGGAAATGA	3400
AL137471	1698	CGATGAGGACACTGGGGATACCAGCACATCATCTCTGCTCTCGGAAATGA	1747
T416	3401	GCAGTGTGTTCCAGCGTCTCTTACCGCCTTCCCTGGACACCTATTCTGAA	3450
AL137471	1748	GCAGTGTGTTCCAGCGTCTCTTACCGCCTTCCCTGGACACCTATTCTGAA	1797

FIG. 4F

T416	3451	TGCAGTGAGGTGGATCGGTCCAACTCCCTGGAGCGCAGGAAGGACCCCTT	3500
AL137471	1798	TGCAGTGAGGTGGATCGGTCCAACTCCCTGGAGCGCAGGAAGGACCCCTT	1847
T416	3501	GCCAGCCAAAACCTGTGGGTTACCCACAGGGGGTAGCGGCATGGGCAGCCA	3550
AL137471	1848	GCCAGCCAAAACCTGTGGGTTACCCACAGGGGGTAGCGGCATGGGCAGCCA	1897
T416	3551	GTACGCATTTTCAAAATCCACCAACCACTGTGGGCCGCCACTTTGGAAC	3600
AL137471	1898	GTACGCATTTTCAAAATCCACCAACCACTGTGGGCCGCCACTTTGGAAC	1947
T416	3601	CACTCCAGTGTGCAGCCTTCTTCAAAATGGCTGCCAGCCATGGAGGAGAT	3650
AL137471	1948	CACTCCAGTGTGCAGCCTTCTTCAAAATGGCTGCCAGCCATGGAGGAGAT	1997
T416	3651	CCCTGAAAATTTATGAGGAAGATGATTTTGACAATGTGCTCAACCACCTCA	3700
AL137471	1998	CCCTGAAAATTTATGAGGAAGATGATTTTGACAATGTGCTCAACCACCTCA	2047
T416	3701	ATGATGGGAAACACGAACTCATGGATGCCAGTGAACCTGGTGGCAGAGATT	3750
AL137471	2048	ATGATGGGAAACACGAACTCATGGATGCCAGTGAACCTGGTGGCAGAGATT	2097

FIG. 4G

T416	3751	AACTGCTTCAAGATGTC	CCG	CAGCTAGGAGATTTTAGCGAAGCA	3800
AL137471	2098	AACTGCTTCAAGATGTC	CCG	CAGCTAGGAGATTTTAGCGAAGCA	2147
T416	3801	TTTTTGTTC	ATGTATATG	GAATAGGAAACAACAACAAAAAA	3850
AL137471	2148	TTTTTGTTC	ATGTATATG	GAATAGGAAACAACAACAAAAAA	2197
T416	3851	CCCTGAAAGAACTGGCA	TTGCCAAATAGTTGCA	TTTATCATAAATGTGTC	3900
AL137471	2198	CCCTGAAAGAACTGGCA	TTGCCAAATAGTTGCA	TTTATCATAAATGTGTC	2247
T416	3901	TGTGTATATTGAATATTAA	ATACTGTATTTTCGTATGTACACA	AAATGCAAG	3950
AL137471	2248	TGTGTATATTGAATATTAA	ATACTGTATTTTCGTATGTACACA	AAAAAAA	2297
T416	3951	TGTGATTATTTTAATCTGTAT	TTTAAAAATACATTTGTACCTTATATTA		4000
AL137471	2298	AAAAAAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAG	2338

FIG. 4H

T416	1	..ATGCACCAATG..AATGCTAAAATGCACCTTTAGGTTTGTGTTTGGCA	45
m-PC	1	ATGATGCTACTTCTGCCATTCCCTGCTAGGGCTCTTAGGGCCAGGAAGCTA	50
T416	46	CTTCTGATAGTATCTTTCAACCCACGATGTA	92
m-PC	51	CT..TGTTCA	98
T416	93	ATACAGGATTTATGAGGAACAGAGGGTTGGATCAGTAATTGCAAGACTAT	142
m-PC	99	ATTCCAAGTGACAGAGGAAGTGCCGTCTGGCACGGTGATAGGGAAACTGT	148
T416	143	CAGAGGATGTGGCTGATGTTTATTGAAGCTTCCCTAAATCCTTCTACTGTT	192
m-PC	149	CCCAAGAACT..AAGA.GTGGAGGAGAGGCGTGGGAAGGCAGGAGATG..	193
T416	193	CGATTTTCGAGCCATGCAGAGGGGAAATTCCTCTACTTGTAGTAAACGA	242
m-PC	194	CCTTCCAGATTCTGCAGCTGCCCTCAGGCACCTGCCGTTTCAGATGA	242

FIG. 5A

T416	243	GGATAATGGGAAATCAGCATAGGGCTACAAATTGACCGTGAACAACTGT	292
m-PC	243	TTGAGACGGCCTGCTCAGCACTTCCAGCCGGCTGGATCGGAGAAGCTAT	292
T416	293	GCCAGAAAACCTTGAACTGTTCCATAGAGTTTGATGTGATCACTCTACCC	342
m-PC	293	GTCGGCAGGAAGATCCCTGTCTGGTGTCAATTGACGTG.....CTTGCC	336
T416	343	ACA.GAGCATCTGCAGCTTTTCCATATTTGAAGTTGAAGTGCTGGATATTA	391
m-PC	337	ACAGGGCGTCTGC.TCTAATTCAATGTGGAGATTCAGGTGCTAGACATCA	385
T416	392	ATGACAAATTCCTCCCAAGTTTTCAGATCTCTCATACCTATTGAGATATCT	441
m-PC	386	ATGACCACCAAGCCACAGTTTCCCAAGACGAGCAGGAACCTGGAAATCTCA	435
T416	442	GAGAGTGCAGCAGTTGGGACTCGCATTCCTCCCTGGACAGTGCAATTTGATCC	491
m-PC	436	GAGAGTGCCCTCTCTGCACACACAGAAATCCCTTTGGACAGAGCTCTTGACCA	485

FIG. 5B

T416	492	AGATGTTGGGGAATAATCCCTCCACACATACTCGCTCTCTGCCAATGATT	541
m-PC	486	AGACACGGGTCCTAACAGCTTATATTCCTACTCCCTGTCTCCCAAGTGAAC	535
T416	542	TTTTTAATATCGAGGTTCCGACCAGGACTGATGGAGCCCAAGTATGCAGAA	591
m-PC	536	ACTTTGCCCTGGATGTTATTGTGGGCCCTGATGAGACCAAAACATGCAGAG	585
T416	592	CTCATAGTGGTCAGAGAGTTAGATCGGGAGCTGAAGTCAAGCTACGAGCT	641
m-PC	586	CTTGTGGTGGTGAAGGAGTTGGACAGGGAACCTCCACTCATATTTTGATCT	635
T416	642	TCAGCTCACTGCCCTCAGAC.ATGGGAGTACCTCAGAGGTCTGGGCTCATCC	690
m-PC	636	GGTGTGACCGCCCTATGACAAATGGGAAT.CCCCCTAAGTCAGGAATCAGC	684
T416	691	ATACTAAAAATAAGCATTTTCAGACTCCAATGACAAACAGCCCTGCTTTTGA	740
m-PC	685	GTGGTCAAGGTCAATGTCTCTGGACTCCAATGACAAATAGTCCAGTGTTC	734

FIG. 5C

T416	741	GCAGCAATCTTATATAAATACTCTTAGAAAACCTCCCGGTTGGCACTT	790
m-PC	735	TGAGAGTTCACCTAGCACTAGAAAATCCAGAAAGACACTGTTCCTGCTACTC	784
T416	791	TGCTCTTAGATCTGAATGCCACGGATCCAGATGAGGGCGCTAATGGAAA	840
m-PC	785	TTCTCATAAACCTGACTGCTACAGATCCCAGACCAAGGACCCAATGGGGAG	834
T416	841	ATTGTATATTCCTTCAGCAGTCA TGCTCTCCCAAAATATGAGACTTT	890
m-PC	835	GTAGAGTTCTTCTTTGGCAAGCATGTGTCCCCAGAGGTGATGAACACCTT	884
T416	891	TAAAAATTGATTCTGAAGAGGACATTTGACTCTTTTCAAGCAAGTGGA TT	940
m-PC	885	TGGCATAGATGCCCAAGACAGGCCAGATCATTTCTGCGCCAAGCCCTAGATT	934
T416	941	ATGAAATCACCAAATCCTATAGAGATTGATGTTTCAGGCTCAAGATT TGGGT	990
m-PC	935	ACGAGAAGAACCCTGCCTATGAGGTGGATGTCCAGGCAAGGATT TGGGT	984

FIG. 5D

T416	991	CCAAATTCAATCCAGCCCATTCGAAAAATTATAATTAAAGTTGTGGATGT	1040
m-PC	985	CCCAATTCCATCCAGGCCATTGCAAAGTTCTTATCAAAAGTTCTGGATGT	1034
T416	1041	TAAATGACAAATAAACCTGAAATTAAACATCAACCTCATGTCCCCTGGAAAAAG	1090
m-PC	1035	CAATGACAAATGCCCC.....AAGCATCCTCATCACGT....GGCCCTCC	1074
T416	1091	AAGAAATATCTTATATTTTGAAGGGGATCCTATTGATACATTTGTTGCT	1140
m-PC	1075	CAGACGTCGCT..GGTGTCAAGAAAGATCTTCCAGGGATAGCTTCATTGCC	1122
T416	1141	TTGGTCAGAGTTCAGGACAAGGATTCTGGGCTGAATGGAGAAATAGTTTG	1190
m-PC	1123	CTTGTCAAGTGCGAATGACTTGGACTCAGGAAACAACGGTCTCGTCCACTG	1172
T416	1191	TAAGCT...TCATGGACATGGTCACCTTAAACTTCAGAAAGACATATGAAA	1237
m-PC	1173	TTGGCTGAATCAAGAGCTGGGCCACTTCAGACTGAAAAGGACTAACGGCA	1222

FIG. 5E

T416	1238	ACAATTATTAACTTAACTAAATGCCACACTGGATAGAGAAAAGAGATCT	1287
m-PC	1223	ACACGTACATGCTGCTCACCAATGCCACACTGGACAGAGAGCAGTGGCCC	1272
T416	1288	GAGTATAGTTTGACTGTAAATCGCTGAGGACAGGGGACACCCAGTC..TC	1335
m-PC	1273	ATATATACTCTCACTGTGTGTTTGCCCAAGAC.CAAGGAC.CCCAGCCCTTA	1320
T416	1336	TCTACAGTGAAACATTTTACAGTTCAAATCAATGATATCAATGACAATCC	1385
m-PC	1321	TCAGCTGAGAAGGAGCTCCAAATTCAGGTTAGTGATGTCAATGACAATGC	1370
T416	1386	ACCCCACTTCCAGAGAAGCCGATATGAATTTGTAAATTCAGAAAATAACT	1435
m-PC	1371	CCCTGTGTTTGAGAAAGAGCCGGTACGAGGTCTCCACTTGGGAAAATAACC	1420
T416	1436	CACCAGGGGCATATATCACCACCTGTACAGCCACAGATCCTTGATCTTGGGA	1485
m-PC	1421	CACCCTCTCTTCACCTCATCAGCTCAAAGCGCATGATGCTGACTTGGGC	1470

FIG. 5F

T416	1486	GAAAATGGGCAAGTGACATACACCATCTTGGA.GAGTTTATTCT.AGGA	1533
m-PC	1471	AGTAATGGAAAAGTGTATACCGTATCAAGGACTCCCCCGTTTCTCACTT	1520
T416	1534	AGTTCATAACTACATATGTAACCATTTGA...CCCATCTAATGGAGCCAT	1580
m-PC	1521	AGT..CATTATTGACTTTTGAAACAGGAGAAGTCACTGCTCAGAGGTCACT	1568
T416	1581	...CTATGCC...TCAGAAATCTTTGA..TC...ATGA.AGAAGTGAGTC	1618
m-PC	1569	GGACTATGAACAGATGGCAGGCTTTGAGTTCCAGGTGATAGCAGAG.GAC	1617
T416	1619	AGATCAC.TTTTGTGGTAGAAGCAAGAGATGGAGGAAGCCCGAAGCAACT	1667
m-PC	1618	AGAGGGCAACCCAGCTCGCATCCAG.CATCTCGGTGTGGTTAGCCCTCT	1666
T416	1668	GGTAAGC.....AATACCACAGTTGTG.CTCACC.....ATCATTTGAC	1704
m-PC	1667	TGGATGCCCAATGATAATGCCCCCAGAAAGTGATTGAGCCCTGTGCTCAGTGAA	1716

FIG. 5G

T416	1705	GAAAATGACAACGTTCTGTGGTTATA.....GGGCC.....	1736
m-PC	1717	GGCAAAGCCACCCCTTTCGGTGTCTGTAAATGCCCTCCACGGGCCACCTTCT	1766
T416	1737	..TG..CATTGCGTA.....AT.AATACGGCAGAAATCACCATTC	1771
m-PC	1767	GTTGCCCATTTGAGAAATCCCAGTGGCATGGATCCAGCAGGTACTGTATAC	1816
T416	1772	..CCAAAGG.GGCTGAAAG....TGG.CTTT.CATGTCACAAGAATAAGG	1812
m-PC	1817	CACCAAAGGCTACCCACAGCCCCCTGGTCTTTCCTTTTGTAAACAATCGTG	1866
T416	1813	GCAATTGACAGAGACTCTGGTGTGAATGCTGAACCTCAGCTGCGCCATAGT	1862
m-PC	1867	GCTAGGGATGCAGACTCGGGGCCAATGGGGAACCTTCTACAGCATTCA	1916
T416	1863	AGCAGGTAATGAGGAGAAATATCTTCATAATTGATCCACGATCATGTGACA	1912
m-PC	1917	AAGTGGGAATGATGCTCATCTCTT.TTTCCTCAGCC.CTTCCCTTGGGGCA	1964

FIG. 5H

T416	1913	TCCAT..ACCAACGTTAGC.ATGGATTCTGTTCCCTACACAG..AATGGG	1957
m-PC	1965	GCTATTCAATTAAATGTCACCAATGCCAGCAGCCTCATCGGAGTCAGTGGG	2014
T416	1958	AGCTGTCAGTTATCATTCAGGACAAAGGCAATCCTCAGCTACATACCAA	2007
m-PC	2015	ACCTGGGATAGTGGTAGAGGACCAGGGCAGCCCTCCTTGCAGACCCAA	2064
T416	2008	GTCCTTCTGAAGTGCATGATCTTTGAAATATGCAGAGTCGGTGACAAGTAC	2057
m-PC	2065	GTTTCATTGAAGGTCGTG...TTTG..TCACCAGTGT..GGACCACCTAA	2107
T416	2058	AGCAATGACTTCAGTAAGCCAGGCATCCTTGGATGTCCTCCATGA.TAATA	2106
m-PC	2108	GGGATTCTGCTCA.TGAGCCCGGAGTTCT..GAGCACACCAGCAGTGGCT	2154
T416	2107	ATTATTTCCTTAGGAGCAATTGTGCAGTGTGCTGGTTATTATGGTGCT	2156
m-PC	2155	TTGATCTGCCCTGGCTGTACTGCTGGCCATCTTTGGATTGCTCTTAGCCCT	2204

FIG. 5I

T416	2157	ATTGCAACTAGGTGTAACCGCGAGAGAAAGACACTAGATCCTATAACT	2206
m-PC	2205	GTTCGTGTCCATCTGCAGGACAGAGAGAAAGGATAATAGGGCCTACAAC	2254
T416	2207	GCAGGGTGGCCGAATCAACTTACCAGCACCCCAAAAGGCCATCCCGG	2256
m-PC	2255	GTCGAGAAAGCTGAGTCGTCTATACCGCCACCAGCCCAAGAGGCCCCAGAAA	2304
T416	2257	CAGATTCACAAAGGGGACATCACATTGGTGCCCTACCATAAATGGCACTCT	2306
m-PC	2305	CACATTCAGAAGGCAGATATCCACCTGGTGCCCTGTGCT.TAGGGCCCCAC.	2352
T416	2307	GCCCATCAGATCTCATCA...CAGATCGTCTC.CATCTTCATCTCCTA..	2350
m-PC	2353	GAGAAATGAGA.CTGATGAAGTCAGGCCCATCTCACAAGGATACCAGCAAGG	2401
T416	2351	..CCTTAGAAAGAGGGCAGATGGG.....CAGCCGGCAGAGTCACAA	2390
m-PC	2402	AGACACTGATGGAGGCAGGCTGGGACTCTTGCCCTGGAGGCCCCCTTCCAC	2451

FIG. 5J

T416	2391	CAGTCACCAGTCACTCAACAGTTTGGTGACAATCTCATCAAACCACG...	2437
m-PC	2452	CTCACACCA.ACCCTATACAGGACCCCTGCGTAACCAAGGCAACCAGGGAG	2500
T416	2438	...TGCCAGA.....GAAATTCT.CATTAGAAC.TCACC...CACGCC	2472
m-PC	2501	AACTGGCAGAGAGCCAGGAGGTACTGCAGGACACCTTCAACTTCTCTTT	2550
T416	2473	ACTCCTGC..TGTTGA.GCAGGTCTCTC...AGCTTCT....TTCAATGC	2512
m-PC	2551	AACCATCCAGGCAGAGGAATGCCTCCCGGAGAACCTAAACCTTCCTGA	2600
T416	2513	TTCAACCAGGGCAATA..TCAGCCAAGACCAAG..TTTTCGAGGAAACAA	2558
m-PC	2601	GTCCCCACCTGCTGTACGCCAACCACTCTTAAGGCCCTCTGAAGGTGCCCTG	2650
T416	2559	ATATTCCAGGAGCTACAGATA.TGCCCTTCAAGACATGGACAAATTTAGC	2607
m-PC	2651	GTAGCCCCATAGCGAGGGCGACTGGAGACCAAGACAAAGGAGGA....GGC	2696

FIG. 5K

T416	2608	TTGAAAGACAGTGGCCGTGGTGACAGTGAGGC..AGGAGACAG.TGATTA	2654
m-PC	2697	CCCACAGAGCCCAACAGCGTCTCTGCAACCCCTAAGACGACAGCGGAATT	2746
T416	2655	TGATTTGGGGCGAGATTCTCCAATA.GATAGGCTGCTGGGTGAAGGATTTC	2703
m-PC	2747	TCAAT..GGCAAAGTGTCTCCTAGAGGAGAGTCCGGTCTCTCATCAGATTTC	2794
T416	2704	..AGCGACCTGTTT...CTCACAGATGGAAGAAATTCAGCAGCAGCTATGAGA	2748
m-PC	2795	TGAGGAGCCTGGTTAGGCTCTCTG.TGGCTGCTTTTGCGGA...ACGGAA	2840
T416	2749	CTCTGCACGGAGGAG..TGCAGGGTCCTGGGACACTCTGACCAGTGCTGG	2796
m-PC	2841	CCCGG..TGGAGGAGCCTGCTGGGACT..CTCCTCTGTCCAGCAAATC	2886
T416	2797	ATGCCACCACTGCCCTCAC....CGTCTTCTGATTATAGGAGTAACATGT	2842
m-PC	2887	TCCCAGCTGCTGTCTGCTGTCACCAAGGGCCAATTCACAGCCCAACCAAA	2936

FIG. 5L

T416	2843	TCATTCCAGGGGAAGAATTCCCAACGCCACCCAGCAGCAGCATC.....	2887
m-PC	2937	CCA..CCGAGGAAATAAATACTTGCCCAAGCCCGCGCAGCAGCAGGGG	2984
T416	2888	.CACATCAGAGTC.TTGAGGATGACGCTCAGCCTGCAGATTCCGGTGAAA	2935
m-PC	2985	TACCATCCAGACACAGAGGGCCTTG.TAGGCCTCAAGCCT.AGTGGCCA	3032
T416	2936	.AGAAGAAGAGTTTTTCCACCCTTTGGAAAGGACTCCCCAAACGATGAGGAC	2985
m-PC	3033	AGCAGAA.....CCTGACCCTGGAAGAAGGGC.CCCCGAGCCCGGAGGA.	3074
T416	2986	.ACTGGGGATACCAGCACATC.ATCTCTGCTCTCGGAAATGAGCAGTGTGT	3034
m-PC	3075	...GGACCTTTCTGTAAAGCGACTTCTAGAAGAAGAGCTGTCGAGCCTGT	3121
T416	3035	.TCCAGCGTCTCTTACCGCCTTCCCTGGACA..CCTATTCTGAATGCAGTG	3082
m-PC	3122	TGGACCCCTAATACAGGTCTAGCCCTTGGACAAGCTGAGTCCGCCTGACCCA	3171

FIG. 5M

T416	3083	AGGTGGATCG.GTCCAAC	TCCCTGGAGCGCAGGAAGGACCC	TTGCCAGC	3131
m-PC	3172	GCCTGGATGGCGAGATTGTCAT	TGCCCCCTCA.....CCACCAATTATCGA	3216	
T416	3132	CAAAACTGTGGGTTACCCACAGGGG	TAGCGGCATGGGCAGCCAGTACGC	3181	
m-PC	3217	GACAACT.TGTCTTCCCCCGATGCTACAACATCAGAGGAACCGAGAAC..	3263		
T416	3182	ATTTTCAAAAATCCCAACCACTGTGGCCGCCACTTGGAAC	TCACTCC	3231	
m-PC	3264	.CTTCCAGACATTTCGGCAAGACAGTTGGACCGGGAC.CCGAGCTGAGCCC	3311		
T416	3232	AGTGTGCAGCCCTTCTTCAAAATGGCTGCCAGCCATGGAGGAGATCCCT..	3279		
m-PC	3312	AACAGGCACGGCCTGGCCAGCACTTTCGTCTCGGAGATGAGCTCTCTGC	3361		
T416	3280	..GAAA..ATTATGAGGAAGATGATTTTGACAA	TG..TGCT.CAACCACC	3322	
m-PC	3362	TGGAATGTTGTTGGGGCAGCACACGGTACCAAGTGGAAAGCTGCGTCCGCG	3411		

FIG. 5N

T416	3323	TCAATGATGGGAAACACGAACTCATGGATG....CCAGT...GA.....	3359
m-PC	3412	GCTTTGCGGAGGCTCTCGGTGTGCGGAGGACCCCTCAGTCTAGACCTAGC	3461
T416	3360ACTGGTGGCAGAGATTAA...ACTGCTT..CAAGATGTCCGC.C	3400
m-PC	3462	CACCAAGTGGGGCTTCAGCTTCAGAAAGCACAGGTAGAAAGAGGCAGCTG	3511
T416	3401	AGAGC.....	3405
m-PC	3512	AGAGCAGACTTGGCTGTGGCAGGAATCTA	3540

FIG. 50

m-PC	1	MMLLLPFLGLLGPGLSGLFISGDCQEVATVMVKFQVTEEVPSGTVIGKLS	50
T416	1	.MHQMNAKMHFRFVFALLIVSFN.HDVLGKNLKYRIYEEQRVGSVIARLS	48
m-PC	51	QELR..VEERRGKAGDAFQILQLPQALPVQMNSDGLLSTSSRLDREKLC	98
T416	49	EDVADVLLKLPNPSTVFRAMQRGNSPLLVVNEDNGEISIGATIDREQLC	98
m-PC	99	RQEDPCLVSDV..LATGASALIHVEIQVLDINDHQPPQFPKDEQELEISE	146
T416	99	QKNLNCSEFDVITLPTTEHLQLFHIEVEVLDINDNSPQFSRSLPIEISE	148
m-PC	147	SASLHTRIPLDRALDQDTGPNLSYSLSLSPSEHFALDVI VGPDETKHAEL	196
T416	149	SAAVGTRIPLDSAFDPDVGENSLHTYLSLSANDFFNIEVRTRTDGAKYAEL	198
m-PC	197	VVKELDRELHSYFDLVLTAYDNGNPPKSGISVVKVNVLDNSDNDNSPVFAE	246
T416	199	IVVRELDRELKSSYELQLTASDMGVQPQRSGSSILKISISDSNDNSPAFEQ	248

FIG. 6A

m-PC	247	SSLALEIPEDTVPGTLLINLTATDPDQGPNGEVEFFFGKHVSPEVMNTFG	296
T416	249	QSYIIQLENSPVGTTLLDLNATDPDEGANGKIVYSFSSHVSPKIMETFK	298
m-PC	297	IDAKTGQIILRQALDYEKNPAYEVDVQARDLGPNSIPGHCKVLIKVLDVN	346
T416	299	IDSERGHLTLFKQVDYEITKSYEIDVQAQDLGPNSIPAHCKIIIKVVVDVN	348
m-PC	347	DNAPSILITWAS...QTSLVSEDLPRDSFIALVSANDLDSGNNGLVHCW	392
T416	349	DNKPEININLMSPGKEEISYIFEGDPIDTFVALVRVQDKDSGLNGEIVCK	398
m-PC	393	LNQELGHFRLKRTNGNTYMLLTNATLDREQWPIYTLTVFAQDQGPQLSA	442
T416	399	LHGH.GHFKLQKTYENNYLILTNATLDREKRSEYSLTVAEDRGTPSLST	447
m-PC	443	EKELQIQVSDVNDNAPVFEKSRYEVSSTWENNPPSLHLITLKAHDADLGSN	492
T416	448	VKHFTVQINDINDNPPHFQRSRYEFVISENNSPGAYITTVTATDPDLGEN	497

FIG. 6B

m-PC	493	GKVSRIKD.....SPVSHLVIIDFETGEVTAQRSLDYEQMAGFEFQVIA	537
T416	498	GQVTYTILESFILGSSITTYVTIDPSNGAIYALRIFDHEEVSQITFVVEA	547
m-PC	538	EDRGQP.QLASSISVWVSLLDANDNAPEVIQPVLSE GKATLSVLVNASTG	586
T416	548	RDGSPKQLVSNNTTVVLTIIENDNVVPVIGPALRNNTAEITIPKGAESG	597
m-PC	587	HLLLP IENPSGMDPAGTGIPPKATHSPWSFLLTTIVARDADSGANGELFY	636
T416	598FHVTRIRAI DRDSGVNAELSC	618
m-PC	637	SIQSGNDAHLFFLSPSLGQLFINVTNASSLLIGSQWDLGIVVEDQGSPSLQ	686
T416	619	AIVAGNEENIFIIDPRSCDIHTNV.SMDSVPYTEWELSVIIQDKGNPQLH	667
m-PC	687	TQVSLKVV...FVTSVDHLRDSAHEPGVLSTPALALICLAVLLAIFGLLL	733
T416	668	TKVLLKCMIFEYAESVTSTAMTSVSQASLDVSMIIISLGAICAVLLVIM	717

FIG. 6C

m-PC	734	ALFVSI	CRTERK	DNRAYN	CREAES	SYRHQP	KRPQKH	IQAD	IHLV	PVLR	A	783
T416	718	VLFAT	RNCN	REKKD	TRSYN	CRVAE	STYQH	HPKR	PSRQ	IHKG	DITL	767
m-PC	784	HENET	DEV	..PSH	KDTSK	ETLME	AGWD	SCLE	APFH	LTP	TLTY	831
T416	768	TLPIR	SHHR	SSP	SSPT	LERG	QMGS	RQSH	NSHQ	SLNS	LVTI	817
m-PC	832	QGE	LAES	QEV	LQD	TFN	FLFN	HPRQ	RNA	SREN	LNLPE	881
T416	818	SLE	LTHA	TPA	VEQ	VSQ	LLS	MLH	QGQ	YQPR	PSFR	867
m-PC	882	VPG	PIA	RAT	GQD	KEE	APQ	SP	PASS	ATL	RRQ	931
T416	868	FS...	LKD	S	GRGD	SEAG	SDYD	LGRD	SPID	RLLG	EGFSD	913
m-PC	932	LRS	LVR	LSV	AAFA	ERNP	VEEP	AGD	SPV	QIQ	ISQL	981
T416	914	AMR	LCTE	E	CRV	LGH	SDQ	WMP	PLP	SP	SDY	963

FIG. 6D

m-PC	982	GNKYLAKPGSSRG	TIPDTEGLVGL.KPSGQAE	PDL	EEGPPSP	PEEDLSVK	1030		
T416	964	HQLEDDAQPADS	GEKKKSFSTFGK	DSPN	DEDTGDTST	SLLSEMSSVFQ	1013		
m-PC	1031	RLLEEL...	SSLLDPNTGLAL	DKLSPDP	PAWMARLS	PLTTNYRDN	LSS 1077		
T416	1014	RLPPSLD	TYSECSEVDR	NSLER	RKGPLPA	KTVGY	PQGVAAWA	AATHFQ 1063	
m-PC	1078	PDATTSEEP	RTTFQTFGK	TVGPGPEL	SPTGTR	LASTFVSE	MSLLEMLL	GQ 1127	
T416	1064	NPTNCGP	PLGTHS...	SVQPSS	KWLPAMEE	I	PENYEE	DDFDNVLNHLND 1110	
m-PC	1128	HTVPVEA	ASAALRR	LSVCGRT	LSLDLAT	SGASAE	AQGRK	KAESRLGCC	RNL 1180
T416	1111	GKHE	MDASEL	VAEINK	LLQDV	RQS	1135	

FIG. 6E

GAAGTGGGAT	GTGCAAAAGC	GCCGGCTGGA	AATCCCGGCT	GTGTCTCCGT	CAACTCTTTA	60
CGCAACAGAG	GTCTCCCCCT	GCCCTTGTT	TCTACCGGGC	CGCCTGCTCC	CACTCGGCGA	120
AAAAAATTAC	ACAACAGCAG	CCGCGGCG	ATG ACG	TGG AGG	GCT GCC	172
	Met Thr	Trp Arg	Ala Ala	Ala Ser		8
ACG TGC	GCG CTC	CTG ATT	CTG CTG	TGG GCG	CTG ACC	GAA GGT
Thr Cys	Ala Ala	Leu Leu	Ile Leu	Trp Ala	Leu Thr	Thr Glu Gly
						24
GAT CTG	AAA GTA	GAG ATG	GCA GGG	GGG ACT	CAG ATC	ACA CCC
Asp Leu	Lys Val	Glu Met	Met Ala	Gly Thr	Gln Ile	Thr Pro Leu
						40
AAT GAC	AAT GTC	ACC ATA	TTC TGC	AAT ATC	TTT TAT	TCC CAA
Asn Asp	Asn Val	Thr Ile	Phe Thr	Cys Asn	Ile Phe	Tyr Ser
						Gln Pro Leu
						56
AAC ATC	ACG TCT	ATG GGT	ATC ACC	TGG TTT	TGG AAG	AGT CTG
Asn Ile	Thr Ser	Met Gly	Ile Thr	Trp Phe	Trp Lys	Ser Leu
						Thr Phe
						72
GAC AAA	GAA GTC	AAA GTC	TTT GAA	TTT TTT	GGA GAT	CAC CAA
Asp Lys	Glu Glu	Val Lys	Val Phe	Phe Glu	Gly Phe	His Gln
						Glu Ala
						88
TTC CGA	CCT GGA	GCC ATT	GTG TCT	CCA TGG	AGG CTG	AAG AGT
Phe Arg	Pro Pro	Gly Ala	Ile Val	Ser Pro	Trp Arg	Leu Lys
						Ser Gly Asp
						104
GCC TCA	CTG CGG	CTG CCT	GGA ATC	CAG CTG	GAG GAA	GCA GGA
Ala Ser	Leu Arg	Leu Pro	Gly Ile	Gln Leu	Glu Glu	Ala Gly
						Glu Tyr
						120

Fig. 7A

CGA TGT GAG GTG GTG GTC ACC CCT CTG AAG GCA CAG GGA ACA GTC CAG	556
Arg Cys Glu Val Val Val Thr Pro Leu Lys Ala Gln Gly Thr Val Gln	136
CTT GAA GTT GTG GCT TCC CCA GCC AGC AGA TTG TTG CTG GAT CAA GTG	604
Leu Glu Val Val Ala Ser Pro Ala Ser Arg Leu Leu Asp Gln Val	152
GGC ATG AAA GAG AAT GAA GAC AAA TAT ATG TGT GAG TCA AGT GGG TTC	652
Gly Met Lys Glu Asn Glu Asp Lys Tyr Met Cys Glu Ser Ser Gly Phe	168
TAC CCA GAG GCT ATT AAT ATA ACA TGG GAG AAG CAG ACC CAG AAG TTT	700
Tyr Pro Glu Ala Ile Asn Ile Thr Trp Glu Lys Gln Thr Gln Lys Phe	184
CCC CAT CCC ATA GAG ATT TCT GAG GAT GTC ATC ACT GGT CCC ACC ATC	748
Pro His Pro Ile Glu Ile Ser Glu Asp Val Ile Thr Gly Pro Thr Ile	200
AAG AAT ATG GAT GGC ACA TTT AAT GTC ACT AGC TGC TTG AAG CTG AAC	796
Lys Asn Met Asp Gly Thr Phe Asn Val Thr Ser Cys Leu Lys Leu Asn	216
TCC TCT CAG GAA GAC CCT GGG ACT GTC TAC CAG TGT GTG GTA CGG CAT	844
Ser Ser Gln Glu Asp Pro Gly Thr Val Tyr Gln Cys Val Val Arg His	232
GCG TCC TTG CAT ACC CCC TTG AGG AGC AAC TTT ACC CTG ACT GCT GCT	892
Ala Ser Leu His Thr Pro Leu Arg Ser Asn Phe Thr Leu Thr Ala Ala	248
CGG CAC AGT CTT TCT GAA ACT GAG AAG ACA GAT AAT TTT TCC ATT CAT	940
Arg His Ser Leu Ser Glu Thr Glu Lys Thr Asp Asn Phe Ser Ile His	264

Fig. 7B

TGG TGG CCT ATT TCA TTC ATT GGT GTT GGA CTG GTT TTA TTA ATT GTT	988
Trp Trp Pro Ile Ser Phe Ile Gly Val Gly Leu Val Leu Leu Ile Val	280
TTG ATT CCT TGG AAA AAG GTA AGG GGC TCC AAA GCA AAG TTC AGC CCT	1036
Leu Ile Pro Trp Lys Lys Val Arg Gly Ser Lys Ala Lys Phe Ser Pro	296
GTG TCT TGG GCT AGT AAA AAG CTT TTA GAG CAG CTG CTG CCA ACC TTA	1084
Val Ser Trp Ala Ser Lys Lys Leu Leu Glu Leu Leu Pro Thr Leu	312
CAA GCC TCA AGG GAC AGG CCT GCT GGA AAG GAC TTT GTC AGT CCC TCT	1132
Gln Ala Ser Arg Asp Arg Pro Ala Gly Lys Asp Phe Val Ser Pro Ser	328
TCA CCA TCA GGT GTT GGG AAT GTT GGC TGT GTT CCA ATC CAG TTT CCT	1180
Ser Pro Ser Gly Val Gly Asn Val Gly Cys Val Pro Ile Gln Phe Pro	344
ATC ACA GAG GAC CTA GCT GTC ACA TAC CAT CTG ACC TCT GTA TGG TGG	1228
Ile Thr Glu Asp Leu Ala Val Thr Tyr His Leu Thr Ser Val Trp Trp	360
TTT GTG ACT CTG GGG TGATGTGTTG TAAAGCCTCC CTCTCTTTCT CCATACTAAA	1283
Phe Val Thr Leu Gly	365
CAAGTATTAT ATCTCTGTGA ATGAACCAGA CTTTAGTGTT CAGACCAGGC CCTGAACTAT	1343
GTGTGGACTG CTTGTTTTTC TCACACATTT AGAAACTATG GCTTAGAGAG GGAATTCCT	1403
CATATTTTAT CTGATCAATA ACTGACCACC AGATCTCACT AGTTTGACTA AGAATTTCTA	1463
ACCCTCACTA GGTATTCTA AACTAAAACA TGTTTCTAAA CATTTTATC CCTGACTATG	1523

Fig. 7C

GCCCAAATAG	TAAATAAAC	AGCTCAAGCT	TTAGAGGCCC	AAGAGACCTA	TGTAATGTG	1583
TTGGTTAAAA	TAGTTTAGA	TAATAAAAGG	GCCCTCAATT	ATTTATGGGC	CTGTCAAGGC	1643
AAAATCTGCA	CAACAGCCAG	TACATCTCAT	TATAAATAAT	TTAGGAGAAG	TGGAATAATC	1703
AGTCAATTA	GAAAAATGGC	CCTTTATCTA	AAGTTGGCCA	TTTAGATTCA	CGGACTTAT	1763
TCCTGTTGGA	TCTAGGCCAT	GAGAAACTG	GATAAAAAGT	GGTTTTCAAA	TGTTTCTTGT	1823
GGTATTTGTG	ACTGTTGTCA	TATTTCTTGC	CTTCTCTGG	TTCTGATATT	CAGGTGCTAT	1883
TGAGAGAGGA	GGAAGGAAGA	AACTAGTCAG	GCAGGCAGTT	AGGGTGGGCC	CTCAGTCAAA	1943
TTCCCTTCAA	CAAAAGAACA	GCCTGAAAAA	TCAAAC TGCA	GATAAGGGAA	CTTGTACAGG	2003
GGGGCTTGCC	TAAACATGC	CCACAGCCAC	ATACATTAAA	ACAAGGCTAC	ACAGGAGACT	2063
TGCCTAGACA	TGCTCACAAT	AGAAAATTCC	ATCCCCTGAC	ACATGCACAG	TAAGGGGAAC	2123
AAAGCCACAT	GGAGTAACTC	AAGCTAAGGG	CTTGCA TGCA	CACTACGAGG	ATGGGTGGA	2183
GCTACCAGAA	ATGTGTGCCT	TATGCCTTTG	TATTCAGCTG	TGAAAATGGCA	ACCCCTCTTT	2243
GGGCCCCCTC	TCTGCAGTGG	AGTGCTTTCT	TCTTTTGCTT	ATTAAACTTT	CACTTCAACT	2303
TCAAAAAAAA	AAAAAAA	AAAAAAA				2330

Fig. 7D

GAAGTTGAAG	TGAAAGTTTA	ATAAGCAAAA	GAAGAAAGCA	CTCCACTGCA	GAGAGGGGC	2246
GAAGTTGAAG	TGAAAGTTTA	ATAAGCAAAA	GAAGAAAGCA	CTCCACTGCA	GAGAGGGGC	121136
CAAAAAGAGG	GTTGCCATTT	CACAGCTGAA	TACAAAGGCA	TAAAGGCACAC	ATTCTTGGTA	2186
CAAAAAGAGG	GTTGCCATTT	CACAGCTGAA	TACAAAGGCA	TAAAGGCACAC	ATTCTTGGTA	121196
GCTCCACCCC	ATCCTCGTAG	TGTGCATGCA	AGCCCTTAGC	TTGAGTTACT	CCATGTGGCT	2126
GCTCCACCCC	ATCCTCGTAG	TGTGCATGCA	AGCCCTTAGC	TTGAGTTACT	CCATGTGGCT	121256
TTGTTCCCCCT	TACTGTGCAT	GTGTCAGGGG	ATGGAATTTT	CTATTGTGAG	CATGTCTAGG	2066
TTGTTCCCCCT	TACTGTGCAT	GTGTCAGGGG	ATGGAATTTT	CTATTGTGAG	CATGTCTAGG	121316
CAAGTCTCCT	GTGTAGCCTT	GTTTAAATGT	ATGTGGCTGT	GGCATGTTT	TAGGCAAGCC	2006
CAAGTCTCCT	GTGTAGCCTT	GTTTAAATGT	ATGTGGCTGT	GGCATGTTT	TAGGCAAGCC	121376
CCCCGTGACA	AGTTCCCTTA	TCTGCAGTTT	GATTTTTCAG	GCTGTTCTTT	TGTTTGAAGG	1946
CCCCGTGACA	AGTTCCCTTA	TCTGCAGTTT	GATTTTTCAG	GCTGTTCTTT	TGTTTGAAGG	121436

Fig. 9A

AATTGACTG	AGGGCCCACC	CTAACTGCCT	GCCTGACTAG	TTTCTTCCTT	CCTCCTCTCT	1886
AATTGACTG	AGGGCCCACC	CTAACTGCCT	GCCTGACTAG	TTTCTTCCTT	CCTCCTCTCT	121496
CAATAGCACC	TGAATATCAG	AACCAGAGAA	AGGCAAGAAA	TATGACAACA	GTCACAAAATA	1826
CAATAGCACC	TGAATATCAG	AACCAGAGAA	AGGCAAGAAA	TATGACAACA	GTCACAAAATA	121556
CCACAAGAAA	CATTGAAAA	CCACTTTTTA	TCCAGTTTTT	TCCAGTTTTT	GATCCAAACAG	1766
CCACAAGAAA	CATTGAAAA	CCACTTTTTA	TCCAGTTTTT	TCCAGTTTTT	GATCCAAACAG	121616
GAATAAGTCC	CGTGAATCTA	AATGGCCAAC	TTTAGATAAA	GGGCCATTTT	TCTTAAATTGA	1706
GAATAAGTCC	CGTGAATCTA	AATGGCCAAC	TTTAGATAAA	GGGCCATTTT	TCTTAAATTGA	121676
CTGATTATTC	CACCTCTCCT	AAATTATTTA	TAATGAGATG	TACTGGCTGT	TGTGCAGATT	1646
CTGATTATTC	CACCTCTCCT	AAATTATTTA	TAATGAGATG	TACTGGCTGT	TGTGCAGATT	121736
TTGCCCTTGAC	AGGCCCATAA	ATAATTGAGG	GCCCTTTTAT	TATCTAAAAC	TATTTTAACC	1586
TTGCCCTTGAC	AGGCCCATAA	ATAATTGAGG	GCCCTTTTAT	TATCTAAAAC	TATTTTAACC	121796

Fig. 9B

AACACATT	CATAGGCTCT	TTGGGCCTCT	AAAGCTTGAG	CTGTTTATT	TACTATTGG	1526
AACACATT	CATAGGCTCT	TTGGGCCTCT	AAAGCTTGAG	CTGTTTATT	TACTATTGG	121856
GCCATAGTCA	GGGATAAAAA	TGTTTAGAAA	CATGTTTAG	TTTAGAAAATA	CCTAGTGAGG	1466
GCCATAGTCA	GGGATAAAAA	TGTTTAGAAA	CATGTTTAG	TTTAGAAAATA	CCTAGTGAGG	121916
GTTAGAAAATT	CTTAGTCAAA	CTAGTGAGAT	CTGGTGGTCA	GTTATTGATC	AGATAAAATA	1406
GTTAGAAAATT	CTTAGTCAAA	CTAGTGAGAT	CTGGTGGTCA	GTTATTGATC	AGATAAAATA	121976
TGAGGAATTC	CCCTCTCTAA	GCCATAGTTT	CTAAATGTGT	GAGAAAAACA	AGCAGTCCAC	1346
TGAGGAATTC	CCCTCTCTAA	GCCATAGTTT	CTAAATGTGT	GAGAAAAACA	AGCAGTCCAC	122036
ACATAGTTCA	GGGCCTGGTC	TGAACACTAA	AGTCTGGTTC	ATTCACAGAG	ATATAATACT	1286
ACATAGTTCA	GGGCCTGGTC	TGAACACTAA	AGTCTGGTTC	ATTCACAGAG	ATATAATACT	122096
TGTTTAGTAT	GGAGAAAGAG	AGGAGGGCTT	TACAACACAT	CACCCACAGAG	TCACAAAACCA	1226
TGTTTAGTAT	GGAGAAAGAG	AGGAGGGCTT	TACAACACAT	CACCCACAGAG	TCACAAAACCA	122156

Fig. 9C

CCATACAGAG	GTCAGATGGT	ATGTGACAGC	TAGGTCCTCT	GTGATAGGAA	ACTGGATTGG	1166
CCATACAGAG	GTCAGATGGT	ATGTGACAGC	TAGGTCCTCT	GTGATAGGAA	ACTGGATTGG	122216
AACACAGCCA	ACATTCCCAA	CACCTGATGG	TGAAGAGGGA	CTGACAAAAGT	CCTTTCCAGC	1106
AACACAGCCA	ACATTCCCAA	CACCTGATGG	TGAAGAGGGA	CTGACAAAAGT	CCTTTCCAGC	122276
AGGCCTGTCC	CTTGAGGCTT	GTAAGGTTGG	CAGCAGCTGC	TCTAAAAGCT	TTTTACTAGC	1046
AGGCCTGTCC	CTTGAGGCTT	GTAAGGTTGG	CAGCAGCTGC	TCTAAAAGCT	TTTTACTAGC	122336
CCAAGACACA	GGGCTGAACT	TTGCTTTGGA	GCCCTTACC	TTTTTCCAAG	GAATCAAAAC	986
CCAAGACACA	GGGCTGAACT	TTGCTTTGGA	GCCCTTACC	TTTTTCCAAG	GAATCAAAAC	122396
AATTAATAAA	ACCAGTCCAA	CACCAATGAA	TGAAATAGGC	CACCAATGAA	TGGAAAAATT	926
AATTAATAAA	ACCAGTCCAA	CACCAATGAA	TGAAATAGGC	CACCAATGAA	TGGAAAAATT	122456
ATCTGTCTTC	TCAGTTTCAG	AA				904
ATCTGTCTTC	TCAGTTTCTG	CA				122478

Fig. 9D

GGCCCCGGCAGCTCGGGCTCGGGATCCGTCGAGGGGAGGCCGAGCTTGCCAAGCTGGCGCCAGCGGGGTC	M	V	2
		ATG	77
P G A R G G A L A R A A G R G L L A L			22
CCC GGC GCC CGC GGC GGC GCA CTG GCG GCG GGT GCC GGC CTC CTG GCT TTG			137
L L A V S A P L R L Q A E E L G D G C G			42
CTG CTC GCG GTC TCC GCC CCG CTC CCG CTG CAG GCG GAG GAG CTG GGT GAT GGC TGT GGA			197
H L V T Y Q D S G T M T S K N Y P G T Y			62
CAC CTA GTG ACT TAT CAG GAT AGT GGC ACA ATG ACA TCT AAG AAT TAT CCC GGC ACC TAC			257
P N H T V C E K T I T V P K G K R L I L			82
CCC AAT CAC ACT GTT TGC GAA AAG ACA ATT ACA GTA CCA AAG GGC AAA AGA CTG ATT CTG			317
R L G D L D I E S Q T C A S D Y L L F T			102
AGG TTG GGA GAT TTG GAT ATC GAA TCC CAG ACC TGT GCT TCT GAC TAT CTT CTC TTC ACC			377
S S S D Q Y G P Y C G S M T V P K E L L			122
AGC TCT TCA GAT CAA TAT GGT CCA TAC TGT GGA AGT ATG ACT GTT CCC AAA GAA CTC TTG			437
L N T S E V T V R F E S G S H I S G R G			142
TTG AAC ACA AGT GAA GTA ACC GTC CGC TTT GAG AGT GGA TCC CAC ATT TCT GGC CGG GGT			497

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Fig. 10A

F L L T Y A S S D H P D L I T C L E R A 162
TTT TTG CTG ACC TAT GCG AGC AGC GAC CAT CCA GAT TTA ATA ACA TGT TTG GAA CGA GCT 557

S H Y L K T E Y S K F C P A G C R D V A 182
AGC CAT TAT TTG AAG ACA GAA TAC AGC AAA TTC TGC CCA GCT GGT TGT AGA GAC GTA GCA 617

G D I S G N M V D G Y R D T S L L C K A 202
GGA GAC ATT TCT GGG AAT ATG GTA GAT GGA TAT AGA GAT ACC TCT TTA TTG TGC AAA GCT 677

A I H A G I I A D E L G G Q I S V L Q R 222
GCC ATC CAT GCA GGA ATA ATT GCT GAT GAA CTA GGT GGC CAG ATC AGT AGT GTG CTT CAG CGC 737

K G I S R Y E G I L A N G V L S R D G S 242
AAA GGG ATC AGT CGA TAT GAA GGG ATT CTG GCC AAT GGT GTT CTT TCG AGG GAT GGT TCC 797

L S D K R F L F T S N G C S R S L S F E 262
CTG TCA GAC AAG CGA TTT CTG TTT ACC TCC AAT GGT TGC AGC AGA TCC TTG AGT TTT GAA 857

P D G Q I R A S S S W Q S V N E S G D Q 282
CCT GAC GGG CAA ATC AGA GCT TCT TCC TCA TGG CAG TCG GTC AAT GAG AGT GGA GAC CAA 917

V H W S P G Q A R L Q D Q G P S W A S G 302
GTT CAC TGG TCT CCT GGC CAA GCC CGA CTT CAG GAC CAA GGC CCA TCA TGG GCT TCG GGC 977

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Fig. 10B

Figure 10C

D S S N N H K P R E W L E I D L G E K K 322
 GAC AGT AGC AAC AAC CAC CAC AAA CCA CGA GAG TGG CTG GAG ATC GAT TTG GGG GAG AAA AAG 1037

 K I T G I R T T G S T Q S N F N F Y V K 342
 AAA ATA ACA GGA ATT AGG ACC ACA GGA TCT ACA CAG TCG AAC TTC AAC TTT TAT GTT AAG 1097

 S F V M N N N S K W K T Y K G I V 362
 AGT TTT GTG ATG AAC TTC AAA AAC AAT TCT AAG TGG AAG ACC TAT AAA GGA ATT GTG 1157

 N N E E K V F Q G N S N F R D P V Q N N 382
 AAT AAT GAA GAA AAG GTG TTT CAG GGT AAC TCT AAC TTT CGG GAC CCA GTG CAA AAC AAT 1217

 F I P P I V A R Y V R V V P Q T W H Q R 402
 TTC ATC CCT CCC ATC GTG GCC AGA TAT GTG CGG GTT GTC CCC CAG ACA TGG CAC CAG AGG 1277

 I A L K V E L I G C Q I T Q G N D S L V 422
 ATA GCC TTG AAG GTG GAG CTC ATT GGT TGC CAG ATT ACA CAA GGT AAT GAT TCA TTG GTG 1337

 W R K T S Q S T S V S T K K E D E T I T 442
 TGG CGC AAG ACA AGT CAA AGC ACC AGT GTT TCA ACT AAG AAA GAA GAT GAG ACA ATC ACA 1397

 R P I P S E E T S T G I N I T T V A I P 462
 AGG CCC ATC CCC TCG GAA GAA ACA TCC ACA GGA ATA AAC ATT ACA ACG GTG GCT ATT CCA 1457

Fig. 10C

L	V	L	L	L	V	V	L	V	F	A	G	M	G	I	F	A	A	F	R	K	482
TTG	GTG	CTC	CTT	GTT	GTC	CTG	CTG	GTG	TTT	GCT	GGA	ATG	GGG	ATC	TTT	GCA	GCC	TTT	AGA	AAG	1517
K	K	K	K	G	S	P	P	Y	G	S	A	E	A	Q	K	T	D	C	W	K	502
AAG	AAG	AAG	AAA	GGA	AGT	CCG	TAT	GGA	TCA	GCA	GAG	GCT	CAG	AAA	ACA	GAC	TGT	TGG	AAG	1577	
Q	I	K	Y	P	F	A	R	H	Q	S	A	E	F	T	I	S	Y	D	N	522	
CAG	ATT	AAA	TAT	CCC	TTT	GCC	AGA	CAT	CAG	TCA	GCT	GAG	TTT	ACC	ATC	AGC	TAT	GAT	AAT	1637	
E	K	E	M	T	Q	K	L	D	L	I	T	S	D	M	A	D	Y	Q	Q	542	
GAG	AAG	GAG	ATG	ACA	CAA	AAG	TTA	GAT	CTC	ATC	ACA	AGT	GAT	ATG	GCA	GAT	TAC	CAG	CAG	1697	
P	L	M	I	G	T	G	T	V	T	R	K	G	S	T	F	R	P	M	D	562	
CCC	CTC	ATG	ATT	GGC	ACC	GGG	ACA	GTC	ACG	AGG	AAG	GGC	TCC	ACC	TTC	CGG	CCC	ATG	GAC	1757	
T	D	A	E	E	A	G	V	S	T	D	A	G	G	H	Y	D	C	P	Q	582	
ACG	GAT	GCC	GAG	GAG	GCA	GGG	GTG	AGC	ACC	GAT	GCC	GGC	GGC	CAC	TAT	GAC	TGC	CCG	CAG	1817	
R	A	G	R	H	E	Y	A	L	P	L	A	P	P	E	P	E	Y	A	T	602	
CCG	GCC	GGC	CGC	CAC	GAG	TAC	GCG	CTG	CCC	CTG	GCG	CCC	CCG	GAG	CCC	GAG	TAC	GCC	ACG	1877	
P	I	V	E	R	H	V	L	R	A	H	T	F	S	A	Q	S	G	Y	R	622	
CCC	ATC	GTG	GAG	CGG	CAC	GTG	CTG	CGC	GCC	CAC	ACG	TTC	TCT	GCG	CAG	AGC	GGC	TAC	CGC	1937	

Fig. 10D

Fig. 10E

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AAAACAAGCAAAGAAACAACCTCAGCAGCTGCCCGTTTCCTTAGTCTCCACTTCAGAGGGGGATGCCAAGAGGTCGG 2930
CCCAGCTCCGGTGACCATGAAGGTGGCACAGGAATTACAGTGTGAATGGCTGTGTCAGATGTTTTCGTACCTCAGATTA 3009
AAAATATTGCTGAGGTCAGACGCCACAAATTTTCATGACTTTCCTCAGAAGTAGCACATTTTCGTGACTTCCGCTGTCCCT 3088
CTGAAAAACAAGTTATTTGGAACATGTTCAAGCAAGTCTGACCAAGTCTAAATCGAGCTTTTCTACTGACAT 3167
GAAACTGTTGGAAACTGATCTCAATTTTATAAGAAATGATTTTCCCTCAAGGAGCGCTGTAAATCCAGAACAAGTCCA 3246
GACATCAGCTGTACCTCATGCTCAGTAGTTTATTTAGTTTCTTTTGTGAGTTAACTATGGGAGATTTAACCTCTTT 3325
TGCCAAAAGAGGGAAGTGTGTGTTTTTTAATAGAAAAATATGGACCAAAAATTTTTTCCCTGAAGAATGTATTATAA 3404
CCCTATTTGTGGTTATTACATCCTGTGAAATGTATATATGTTAAAAATAATGGGGGTGCTGGAAGGTCATGGCAGACT 3483
AGCTGCTGGTTAGTGTGGAGGGGAAGTGGTTTACTTTGTAGAGTTTACATGGTTTATGCGCACACTAATTGTAATAAA 3562
CTATGCCAAACCAAAATAAAAAAATAAAAAA

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Fig. 10F

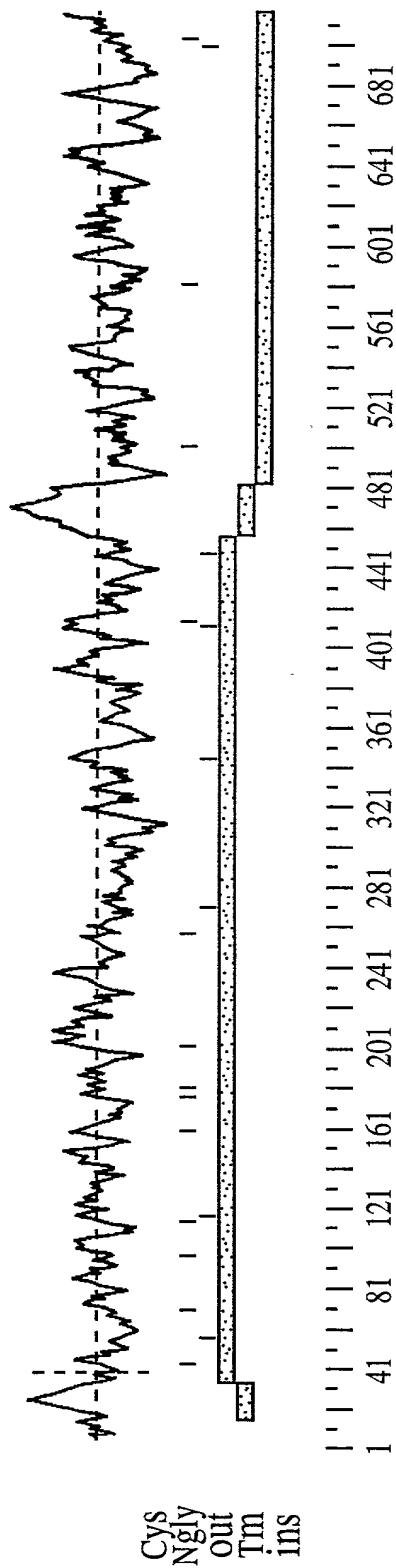


FIG. 10G

Letter "O" Defining

GTGGTCGCGCGAGGTGAGACTGTGAAGAAGAAACGTTGCTTGGGCAAAAGGAGCATATTCTCAGGAGACGGGC	79
CCCTGCGCTGCCACACCAAGCATTAGGCCACCAGGAAGACCCCATCTGTCAAGCAAGCCTAGCCTTCCAGGGAGAAAGAG	158
M N W H M I I S G L I V V V	
GCCCCCTGCAGCTCCTTCATC ATG AAC TGG CAC ATG ATC ATC TCT GGG CTT ATT GTG GTA GTG	14 220
L K V V G M T L F L L Y F P Q I F N K S	34
CTT AAA GTT GTT GGA ATG ACC TTA TTT CTA CTT TAT TTC CCA CAG ATT TTT AAC AAA AGT	280
N D G F T T T R S Y G T V S Q I F G S S	54
AAC GAT GGT TTC ACC ACC ACC AGG AGC TAT GGA ACA GTC TCA CAG ATT TTT GGG AGC AGT	340
S P S P N G F I T T R S Y G T V S Q I F G S S	62/361
TCC CCA AGT CCC AAC GGC TTC ATT ACC ACA AGG AGC TAT GGA ACA GTC TGC CCC AAA GAC	74 400
W E F Y Q A R C F F L S T S E S S W N E	94
TGG GAA TTT TAT CAA GCA AGA TGT TTT TTC TTA TCC ACT TCT GAA TCA TCT TGG AAT GAA	460
S R D F C K G K G S T L A I V N T P E K	114
AGC AGG GAC TTT TGC AAA GGA AAA GGA TCC ACA TTG GCA ATT GTC AAC ACG CCA GAG AAA	520
L K F L Q D I T D A E K Y F I G L I Y H	134
CTG AAG TTT CTT CAG GAC ATA ACT GAT GCT GAG AAG TAT TTT ATT GGC TTA ATT TAC CAT	580

Fig. 11A

R E E K R W R R W I N N S V F N G N V T N 154
CGT GAA GAG AAA AGG TGG CGT TGG ATC AAC AAC TCT GTG TTC AAT GGC AAT GTT ACC AAT 640

Q N Q N F N C A T I G L T K T F D A A S 174
CAG AAT CAG AAT TTC AAC TGT GCG ACC ATT GGC CTA ACA AAG ACA TTT GAT GCT GCA TCA 700

C D I S Y R R I C E K N A K * 188
TGT GAC ATC AGC TAC CGC AGG ATC TGT GAG AAG AAT GCC AAA TGA 745
TCACAGTTCCTGTGACAAGAACTATACTTGCAACTCTTTTGAATCCATACAGGTCGTCTGGCCAAATGATTTTAC 824
TTACCTATCTGTCTACCAAGTAGCGTCTTGGCAATTTGGAAACTGAGCTTCTTCTCTGCACCTGGGGACTGGATG 903
CTAGCCATCTCCAGGAGACAGGATCAGTTTACGGAAACAACCTCAGTTAGTATAGAGATGAGGTCGCTTCTGTAGTAC 982
TGAGCATTTCTGACTGATCAAAAAGGCTAGTCTGTTGACAGGTTTGTGTTTATTTTAGCCTCAGAGTATACCATAC 1061
CTAGGGAGTAACTGTAGAGTGAGAAATATAAATATTTAGGGATTACCATGTTGAAAGAGGGATAAAACATAGGTCC 1140
TGTGACTTCGTCTCTGTTCTCAAGGGAACCCCATTCACATGCCCTCCTAACTCCACAAGCAGGGTAGCAGAGGCTCT 1219
CCTCAGTCTGAACCTAAGGCTTGGCCCTTGGGAGGGCTCCTAGTCTGAGCTTGGAGCAGCACGGACAGCAGCATTTGTTT 1298
ATGGGAATGGAGAGAGGTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAAACCCAGGCAGCCAAAGGAGC 1377
CAACACACTAGATTCTGTTCTTCAGCAAAAGCCCTGAAGAGACACTTAAGCTAAATAATCCCTTGTCTATTTCTGAA 1456
ACTCCATTATAACATATGTAACTCCTTTGTAAACCAAAATTTAGGTAAGCAGGCTTCTTGTCTGAAAGGTTTGTAGTA 1535
CCTGGCTGTATTTGTGAGTATTTTAAATTTTGGATAGTCTCTTAGGCAACAATAATCACAATAATATTCATCCCTTC 1614
AGTTCTGGAGAAAGCCTGATACAGGCACAGCCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTGATCTA 1693
GAACTGTCAGCCCGAAGAGTAGGAAAGAGAGGCTGCTCAGGGAAAACATTGGCTGGGGCACGGAATAAGCAC 1772
ATAGTAAAAAGGGAACATCAGGGTCAAAATGGAATCACCTGAGACAGGAACACAGGAGTTCAATTTGGCCACACTGGAAG 1851
AAAGGCAAGAAAAGAGGAAGACAAGTCTTGGAGTACCTTGGCTGTTCTCCACACTCAAGACATCAGCTATACCTGCT 1930
TGGTGCTAAGAAAGAGAAAAGAGATGCCTTTTGTGTTTGTAGTAAAGAAATAATTAACCATTAAGGAAGACCATGTATAA 2009
AACTGATGGAAATAATAGTCAACCAAGTACAGCACATACCATTTTGTGTCTAATAACAATGTAGCACAGTAATGACTGT 2088

Fig. 11B

ACATGTCAATTGTATGTATACCAACAAGATTGTTGTAAATCATATTTTATTATCAACACATAAGTTCTGCTTCTGCATT 2167
 CCTAGGTTTCATCATTTTGGCTCCTTAGCATGGCCACTTACAATTTTAAACATGAGATAACACATCAGGTGTAGAA 2246
 CTTGCTTGAAGGGAATTACAGAAAGTAATTGTGTTTGAAGTGGGTGAAATTTGAAATTAATATTAGTAGCCGGTGGAG 2325
 ATACAAGTTCTCTGACTGTGTTGGGAAAGGATAAGTGCTACCGTTGAGAAAGGAGAAAGGCTGAGTCTAGGTGGAGAA 2404
 AAATATCAACAGAACTCTAGCCAAAGCAAGCCCAAGAACTCAGACAAACAGAAAGGAAATCCTAATCCTTCTGTTTGA 2483
 GAAGAGAGAACTGTAGTTGCTTCACTTCCCTAATTTCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAATAAGGAGCCCA 2562
 TCTAGTGATTTCTTTAGTAGACAGTTTAAATTTCCCAAGATTAGGAGAAATATGTGGGATTTGGTTTAAAGTTTCAATTTGGGAGAGTTCCCTGGA 2641
 ATGGCCCTGGGTGGAGTGGGAGTAGAGGAAATATGTGGGATTTGGTTTAAAGTTTCAATTTGGGAGAGTTCCCTGGA 2720
 TCCTTGCAAGCTTAGATAAAATGTGATCTTTATTAGTAGCAGTGGCATGCTTTTAAAAAAGGCAATGAAAAATTTA 2799
 GCAAGCCACTGAATTTGAGTTTTCACTTTGTCTAATATGCTGTGTGAATCAGTACAGTTTCTTACCCCTTCTCTTGGT 2878
 CTTAAATTTCTTACTGATAAAATGGGTAGTAATACCTATCTCAAAAAATTTATGACATATTAATAACATTTCCCTCTA 2957
 TGTATCTCAATGGCATTAGACATTAGGAGAAAGCATTTTGTGGAGGATTTGAAAGTTGAGATCTTTCATCCCAAGAGTAGCT 3036
 TTTCAATTTGCTAGAAGCTTAATGTAGGCAAGCCACTTCAATTTTCAGAACTTGTGTTTACTCATTTATAATATGGGAATA 3115
 AAAATTTGTGCAAGTCAGAGAAGGTGCTTAAAAAATGTTGTGGCCAAGCCACATGAGATCAAAAGACACACTTTTCATG 3194
 ACCTCAAAATGTGGGCCAGCCTAGGTCAAGCCCAAGCCCAATCCAACTTAGACTCACGAACAAATCCACCTGAGATCAG 3273
 CAGAGCCACCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAAATAAAAAA 3352
 GTCTCTCGTATAGCAAAATCTAACTGATGCAATCTCCATCTGGCCCTTCATCCTTCTCCCTTTATTGTCCTTTTCGTGTAT 3431
 TGTTCATCCAGCAACCAAGGATGATCTTGTAAAAACATTAACACAGATCTGTCAATCTTMAAAAAAATAAAAAAGCCATGA 3510
 AATTNTAGCAAGCCACTGAAATTTGAGTTTTCACCTTTGGTTTCTAATAATGCTGTGTAATCAGANCAGKTTTCTTACCCT 3589
 TTCTTGGTCTTAATTTCTTACTGATAAAATGGGGTGTAAATACCTATCTCAAAAAATTTATGACATATTARATAACA 3668
 TTCCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTTCATCCAAG 3747
 AAGTAGCTTTTCAATTTGTSTAGAAGCTTAATGTAGGCAAGCCACTTCAATTTTCAGAACTTGTGTTTACTCATTTATAATA 3826
 TGGGAATAAAAAATTTGTGCAAGTCAGAGAAGGTGCTTAAAAATGTTGTGGCCAAGCCACATGAGATCAAAAGACACAC 3905
 TTTTCATGACCTCAAAATGTGGGCCAGCCTAGGTCAAGCCCAAGCCCAATCCAACTTACAGTCAAGCAAAATCCACCT 3984
 GAGATCAGCAGAGCCACCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAA 4063
 AAAAAAAGAA 4074

Fig. 11C

GTG	TCG	CGG	CCG	AGT	GTG	AAG	AAAC	GTG	CTT	GGC	AAAG	GAC	TAT	TCT	CAG	GAC	GGGC	79		
CCCT	GCCT	GCC	ACAC	CAAG	CAATT	AGGCC	ACC	AGGA	AGCCCC	CACT	CTG	CAAG	CAAGCCT	AGCCT	TCC	AGG	AGAA	158		
M N W H M I I S G L I V V V																				
GGC	CTG	CAG	CTC	TTCA	TC	ATG	CAC	ATG	ATC	ATC	TCT	GGG	CTT	ATT	GTG	GTA	GTG	220		
L	K	V	V	G	M	T	L	F	L	L	Y	F	P	Q	I	F	N	34		
CTT	AAA	GTT	GTT	GGA	ATG	ACC	TTA	TTT	CTA	CTT	TAT	TTC	CCA	CAG	ATT	TTT	AAA	AGT	280	
N	D	G	F	T	T	T	R	S	Y	G	T	V	S	Q	I	F	G	S	54	
AAAC	GAT	GGT	TTC	ACC	ACC	ACC	AGG	AGC	TAT	GGA	ACA	GTC	TCA	CAG	ATT	TTT	GGG	AGC	AGT	340
S	P	S	P	N	G	F	I	T	T	R	S	Y	G	T	V	C	P	K	D	74
TTCC	CCA	AGT	CCC	AAC	GGC	TTC	ATT	ACC	ACA	AGG	AGC	TAT	GGA	ACA	GTC	TGC	CCC	AAA	GAC	400
W	E	F	Y	Q	A	R	C	F	F	L	S	T	S	E	S	S	W	N	E	94
TTGG	GAA	TTT	TAT	CAA	GCA	AGA	TGT	TTT	TTT	TTA	TCC	ACT	TCT	GAA	TCA	TCT	TGG	AAT	GAA	460
S	R	D	F	C	K	G	K	G	S	T	L	A	I	V	N	T	P	E	K	114
AAGC	AGG	GAC	TTT	TGC	AAA	GGA	AAA	GGA	TCC	ACA	TTG	GCA	ATT	GTC	AAC	ACG	CCA	GAG	AAA	520
L	K	F	L	Q	D	I	T	D	A	E	K	Y	F	I	G	L	I	Y	H	134
CTG	AAG	TTT	CTT	CAG	GAC	ATA	ACT	GAT	GCT	GAG	AAG	TAT	TTT	ATT	GGC	TTA	ATT	TAC	CAT	580

Fig. 11D

R	E	E	K	R	W	R	W	I	N	N	S	V	F	N	G	K	Y	V	N	154
CGT	GAA	GAG	AAA	AGG	TGG	CGT	TGG	ATC	AAC	AAC	TCT	GTG	TTC	AAT	GGC	AAG	TAC	GTG	AAC	640
M	P	Q	F	P	G	D	L	G	L	L	Q	K	T	K	P	E	I	A	G	174
ATG	CCA	CAG	TTT	CCT	GGG	GAT	CTT	GGT	TTG	CTT	CAA	AAG	ACC	AAA	CCT	GAG	ATT	GCT	GGG	700
F	T	L	E	*																178
TTC	ACC	CTG	GAA	TAG																715
CTCAAA	CGCTG	ACACTT	GACTCT	GTTC	TGCTCT	TTCCTT	CTCCTT	CTCCTT	CTCCTT	CTCCTT	CTCCTT	CTCCTT	CTCCTT	CTCCTT	CTCCTT	CTCCTT	CTCCTT	CTCCTT	CTCCTT	794
GGTCC	TTGCC	CAATTT	GGGAA	ACTG	AGCTT	CTTCT	TCTG	CACTG	GGGGA	CTGG	ATG	GCTAG	CCATC	TCCAG	GAG	ACAG	GA			873
TCAGT	TTACG	GAACA	CACTC	AGTT	AGAT	AGAT	AGAT	AGAT	AGAT	AGAT	AGAT	AGAT	AGAT	AGAT	AGAT	AGAT	AGAT	AGAT	AGAT	952
AGGC	CTAG	CTG	TTG	ACAG	GGT	TTG	TTT	ATTT	AGC	CTC	AGAT	ATAC	CACT	ACT	AGG	AGT	AACT	GT	AG	1031
AAAT	TATA	AAAC	ATTAT	TAG	GGATT	ACC	ATG	TG	GAAG	AGG	ATA	AAAC	ATAG	GT	CTG	ACT	TG	CT	CT	1110
GGAA	CCCC	ATT	CAC	ATG	CCCC	CTC	TAA	CTCA	CAAG	CGAG	GTAG	CAAG	GGCT	CTC	CTC	AGT	CTG	AACT	AG	1189
CCTT	GGG	AGG	GCT	CCT	AGT	GCT	GG	AGC	AGC	AGC	AGC	AGC	AGC	AGC	AGC	AGC	AGC	AGC	AGC	1268
CAGG	ATAG	GAAC	CTT	CTT	GGAG	ACCC	CTT	TGA	AGAA	AAAC	CAGG	CAAG	GGAG	CCAA	ACAC	ACT	AG	AT	TT	1347
TCAG	CAA	AGCC	CTG	AA	GAC	ACTT	AA	GCTA	AAAA	ATCCC	TTG	TCAT	ATTT	CTG	AACT	CCAT	TATA	ACAT	AT	1426
CCTT	TGTA	ACCA	AAAT	TAG	TAG	CAAG	CTT	CC	TTG	CTC	TGA	AGG	TTT	TG	AGT	ACCT	GGCT	GT	AT	1505
TTTAA	AAAT	TTT	GGAT	AGT	CTC	TTAG	GCA	CAATA	ATAC	AAAT	ATAT	ATAT	ATAT	ATAT	ATAT	ATAT	ATAT	ATAT	ATAT	1584
AGGC	ACAG	CCCT	ACT	GAC	CCCA	AGG	AGC	CTG	GC	ACT	GAT	TGG	CA	TGAT	CTA	GA	ACT	GGT	CC	1663
TAGG	AAA	AGAG	AGG	CTG	CTC	AGG	AAAC	AT	TGG	CTGG	GCA	CGGA	ATA	AG	CAC	ATAG	TAAA	AAAG	GAA	1742
TCAAA	TG	AAAT	CAC	CTG	AG	CAAG	AAAC	AGG	AGT	TCAT	TTG	CCCA	CACT	GGA	AGAA	GGCA	AGAA	AGAG	AA	1821
GTCT	TG	AGT	AC	CTG	CTG	TTCT	CCAC	ACT	CACA	AGAC	ATC	AGT	ATAC	TACT	CTG	CTT	GGT	GC	ATA	1900

Fig. 11E

GATGCCCTTTTGTGTTGAGTAAGAAATAATTAACCATATAAGGAAGACCATGTATAAAAATGATGGAAATAATAGTCACC 1979
AAAGTACAGCACATACCATTTTGTGCTAATAACAATGTAGCACAGTAATGACTGTACATGTCATTGTATGTATACCAA 2058
ACAAGATTGTTGTAAATCATATTTTATTACAACACTAAGTTCTGCTTCTGCATTCCTAGGTTTCATCATTTTGGCT 2137
CCTTAGCATGGCCACTTACAAATTTTAAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGA 2216
AGTAATTTGTGTTGAGATGGGTGGAATTTGGAATTATATTAGTAGCCGTGGAGATACAAGTTCTCTGACTGTGTTG 2295
GGAAAGGATAAAGTGTACCCGTTGAGAAAGGGAAGAAAGGCTGAGTCTAGGTGGAGAAAAATATCAACAGAACTCTAGCCA 2374
AAGGCAAGCCCCAGAACTCAGACAAACAGAAAAGGAAATCCTAATCCTTCTGTTTTGAGAAAGAGAACTGTAGTTGCTTC 2453
ACTTCCATTTTCATGACAGAAATACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACA 2532
GTTAAATTTCCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGTGGAGTGGGGA 2611
GTAGATAGGGAATATGTGGGATTTGGTTAAAGTTTCATCATTTGGGAGAGTTCTTGATCCTTGCAAGCTTAGATAAATGT 2690
GATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAAAGGCAATGAAAAATTTAGCAAGCCACTGAATTTGAGTTTT 2769
CACTTTGTTTCTAATATGCTGTGAATCAGTACAGTTTTCTTACCCTTTTCTTGGTCTTAATTTCTTACTGATAAAAT 2848
GGGTAGTAATAACCTATCTCAAAAAATTTATGCACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACAT 2927
TAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAAGAGTAGCTTTTCAATTTGCTAGAAAGCTTAAT 3006
GTAGGCAAGCCACTTCATTTTCAGAACTTGTTTACTCATTTATAATATGGGAATAAAAAATTTGTGCAAGTCAGAGAAG 3085
GGTGCCTTAAAAATGTTGTGGCCAGCCACATGAGATCAAAAGACACACTTTTCATGACCTCAAATGTGGGCCCAGCCTA 3164
GGTCAGCCAAACCCCATCCACCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCTAGATCAGCTGA 3243
AACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAAAATAAAAAAGTCTCTCGTATAGCAAAAATCTAA 3322
CTGATGCAATCTCCATCTGCCCTTCATCCTTCTCCCTTTATTGTCCTTTTCGTGATTTGTTTCATCCAGCAACCAGGATGA 3401
TCTTGTAAAAACATTAAACAGATTCTGTCAKCTTTMAAAAAAAAAGCCATGAAATNTAGCAAGCCACTGAAATTT 3480
GAGTTTTCACTTTGGTTTCTAATATGCTGTGAATCAGANCAGKTTTCTTACCCCTTTCTTGGTCTTAATTTCCCTTACT 3559
GATAAAATGGGTWGTAAATACCTATCTCAAAAAATTTATGCACATATTARATAACATTCCTCTATGTATCTCAATGGCA 3638
TTAGACATTAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAAGAGTAGCTTTTCAATTTGSTAGA 3717

Fig. 11F

AGCTTAATGTAGGCAAGCCACTTCAATTTTCAGAACTTGTCTTACTCATTTATAATATGGGAATAAAATTTGTGCAAGT 3796
 CAGAGAAGGGTGCCCTTAAATAATGTTGTGGCCAAGCCACATGAGATCAAAGACACACTTTTCATGACCTCAAATGTGGGC 3875
 CCAGCCTAGGTGAGCCAAACCCCATCCAAACCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCTAGA 3954
 TCAGCTGAAACTCTAAGCACAAAAATAAAAACCTTATCACTGTAAAAAATAAAAAAATAAAAAA 4018

Fig. 11G

GAGACTGTGAAGAAGAAACGTTGCTTGGGCAAAAGGAGCATATTTCTCAGGAGACGGGGCCCTGCCTGCCACACCA 79
 AGCATTAGGCCACCCAGGAAGACCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAGAGCCCCCTGCAGCTCCTTC 158

M N W H M I I S G L I V V L K V V G 19
 ATC ATG AAC TGG CAC ATG ATC ATC TCT GGG CTT ATT GTG GTA GTG CTT AAA GTT GTT GGA 218

M T L F L L Y F P Q I F N K S N D G F T 39
 ATG ACC TTA TTT CTA CTT TAT TTC CCA CAG ATT TTT AAC AAA AGT AAC GAT GGT TTC ACC 278

T T R S Y G T V C P K D W E F Y Q A R C 59
 ACC ACC AGG AGC TAT GGA ACA GTC TGC CCC AAA GAC TGG GAA TTT TAT CAA GCA AGA TGT 338

F F L S T S E S S W N E S R D F C K G K 79
 TTT TTC TTA TCC ACT TCT GAA TCA TCT TGG AAT GAA AGC AGG GAC TTT TGC AAA GGA AAA 398

G S T L A I V N T P E K L K F L Q D I T 99
 GGA TCC ACA TTG GCA ATT GTC AAC ACG CCA GAG AAA CTG AAG TTT CTT CAG GAC ATA ACT 458

Fig. 11H

D	A	E	K	Y	F	I	G	L	I	Y	H	R	E	E	K	R	W	R	W	119
GAT	GCT	GAG	AAG	TAT	TTT	ATT	GGC	TTA	ATT	TAC	CAT	CGT	GAA	GAG	AAA	AGG	TGG	CGT	TGG	518
I	N	N	S	V	F	N	G	N	V	T	N	Q	N	Q	N	F	N	C	A	139
ATC	AAC	AAC	TCT	GTG	TTC	AAT	GGC	AAT	GTT	ACC	AAT	CAG	AAT	CAG	AAT	TTC	AAC	TGT	GCG	578
T	I	G	L	T	K	T	F	D	A	A	S	C	D	I	S	Y	R	R	I	159
ACC	ATT	GGC	CTA	ACA	AAG	ACA	TTT	GAT	GCT	GCA	TCA	TGT	GAC	ATC	AGC	TAC	CGC	AGG	ATC	638
C	E	K	N	A	K	*														165
TGT	GAG	AAG	AAT	GCC	AAA	TGA														659
TCACAGT	TCCCCTGTGACAAGAACTATACTTGCAACTCTTTTGAATCCATACAGGTCGTCTGGCCAATGATCTTTTAC																			738
TTACCTATCTGTCTACCAAGTAGCGGTCCCTTGCCCATTTGGGAACTGAGCTTCTTCTTGCACTGGGGACTGGATG																				817
CTAGCCATCTCCAGGAGACAGGATCAGTTTACGGAAACAACCTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTAC																				896
TGAGCATTTCTGACTGATCAAAAAGGCCCTAGTCTGTTGACAGGGTTTGTTTTATTTTAGCCTCAGAGTATACCATACTA																				975
CTAGGGAGTAACTGTAGAGTGAGAAATTATAAACATTATTAGGGATTACCATGGTGGAAGAGGGATAAACATAGGTCC																				1054
TGTGACTTCGTCTCTGTTCTCAAGGGAACCCCATTCACATGCCCCCTCCTAACTCCACAAGGAGGGTAGCAGAGGCTCT																				1133
CCTCAGTCTGAACCTAAGGCTTGGCCTTGGGAGGGCTCCTAGTGTGAGCTTGAGCAGCACGGACAGCAGCATTTGTTT																				1212
ATGGGAATGGAGAGAGGTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAAACCCAGGCAGCCAAAGGAGC																				1291
CAACACACTAGATTTCTGTTCTTCAGCAAAAGCCCTGAAGAGACACTTAAGCTAAAAATTTCCCTTGTCTATTTCTGAA																				1370
ACTCCATTATAACATATGTAACTCCTTTGTAAACCAAAATTTAGTAAGCAGGCTTCTTTGCTCTGAAGGTTTGTAGTA																				1449
CCTGGCTGTATTTGTTGAGTATTTTAAAAATTTTGGATAGTCTCTTAGGCAACAAATAATCACAATATATTCATCCCTTC																				1528
AGTTCTGGAGAAAGCCTGATACCAGGCACAGCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTGATCTA																				1607

Fig. 11I

GAACTGGTCCAGCCGCGAAGAGTAGGAAAAAGAGAAGGGCTGCTCAGGGAAACAATTGGCTGGGGCACGGAATAAGCAC 1686
 ATAGTAAAAAGGAACATCAGGGTCAAATGAAAATCACCTGAGACAGGAAACAGGGAGTTCATTTGGCCACACTGGAAG 1765
 AAAGGCAAGAAAGAGGAAACAAAGTCTTGGAGTACCCCTGGCTGTTCTCCACACTCACAAAGACATCAGCTATACTCTGCT 1844
 TGGTGCAATAAGAAAGAGAAAGAGATGCCTTTTGTGTTTGGAGTAAAGAAATAATTAAACCATAAGGAAGACCATGTATAA 1923
 AACTGATGGAATAATAGTACCAAAGTACAGCACATACCATTTTGTGCTAATAACAATGTAGCACAGTAATGACTGT 2002
 ACATGTCATTGTATGTATACCAACAAGATTGTTGTAATCATATTTTATTACAACACTAAAGTCTGCTTCTGCATT 2081
 CCTAGGTTTCATCATTTTTGGCTCCTTAGCATGGCCACTTACAATTTTTTAACATGAGATAACACATCAGGTGTCAGAA 2160
 CTTGCTTGAAAGGAATTACCAGAAAGTAATTGTGTTTGAGATGGGTGGAATTTGGAATTAATATTAGTAGCCGGTGGAG 2239
 ATACAAAGTCTCTGACTGTGTTGGGAAAGGATAAGTGCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGGAGAA 2318
 AAATATCAACAGAACTCTAGCCAAGGCAAGCCCAAGAACTCAGACAAACAGAAAGGAAATCCTAATCCTTCTGTTTTGA 2397
 GAAGAGAACTGTAGTTGCTTCACTTCCCTATTTTCATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACA 2476
 TCTAGTGATTTCTTTAGTAGACAGTTTAATTTCCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCA 2555
 ATGGCCTGGGGTGGAGTGGGAGTAGATAGGGAATATGTGGGATTTGGTTTAAAGTTCAATCATGGGAGAGTTCCTGGA 2634
 TCCTTGCAAGCTTAGATAAATGTGATCTTTATAGATAGCAGTGGCATGCTTTTAAAAAAAAGGCAATGAAAAATTTA 2713
 GCAAGCCACTGAATTGAGTTTTCACCTTGTGTTTCTAATAATGCTGTGAATCAGTACAGTTTCTTACCCTTCTTGGT 2792
 CTTAATTTCCCTTACTGATAAAATGGGGTAGTAATACCTATCTCAAAAAATTAATGCACATATTAAATAACATTCCTCTA 2871
 TGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAGAAGTAGCT 2950
 TTTCAATTTGCTAGAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTGTTACTCATTTATAATAATGGGAATA 3029
 AAAATTTGTGCAAGTCAGAGAAGGTGCCTTAAAAATGTTGTGGCCAAGCCACATGAGATCAAAGACACACTTTTCATG 3108
 ACCTCAAATGTGGGCCAGCCTAGGTCAAGCCACCCCATCCAAACCTTAGACTCACGAAACAAATCCACCTGAGATCAG 3187
 CAGAGCCACCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAACTTATCACTGTAAAAAAAATAAAAAAAA 3266
 GTCCTCGTATAGCAAAAATCTAACTGATGCAATCTCCATCTGGCCTTCATCCCTTCTCCCTTTATTTGTCCTTCGTGTAT 3345
 TGTTCATCCAGCAACCAGGATGATCTTTGTTAAACATTAACAGATTCTGTCAKCTTTMAAAAAAAAAGCCCATGA 3424
 AATTNTAGCAAGCCACTGAATTTGAGTTTTCACCTTTGCTTCTAATATGCTGTGTAATCAGANCAGKTTTCTTACCCT 3503

Fig. 11J

TTCTTGGTCTTAATTCCTTACTGATAAAATGGGGTGWGTAATACCTATCTCAAAAAATTATTGCACATATTARATAACA 3582
 TTCCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAG 3661
 AAGTAGCTTTTCAATTTGSTAGAAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTCTTACTCATTTATAATA 3740
 TGGGAATAAAAAATTTGTGCAAGTCAGAGAAGGTGCCTTAAAAATGTTGTGGCCAAAGCCACATGAGATCAAAGACACAC 3819
 TTTTCATGACCTCAAATGTGGCCAGCCTAGGTAGCCCAACCCCATCCACCTTAGACTCACGAACAAATCCACCT 3898
 GAGATCAGCAGAGCCACCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAA 3977
 AAAAAAA 3985

Fig. 11K

GAGACTGTGAAGAAGAAACGTTGCTTGGGCAAAAGGAGCATATTCTCAGGAGACGGGGCCCTGCCTGCCACACCA 79
 AGCATTAGGCCACCAGGAAGACCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAGAGGCCCTGCAGCTCCTTC 158

M N W H M I I S G L I V V V L K V V G 19
 ATC ATG AAC TGG CAC ATG ATC ATC TCT GGG CTT ATT GTG GTA GTG CTT AAA GTT GTT GGA 218

M T L F L L Y F P Q I F N K S N D G F T 39
 ATG ACC TTA TTT CTA CTT TAT TTC CCA CAG ATT TTT AAC AAA AGT AAC GAT GGT TTC ACC 278

T T R S Y G T V C P K D W E F Y Q A R C 59
 ACC ACC AGG AGC TAT GGA ACA GTC TGC CCC AAA GAC TGG GAA TTT TAT CAA GCA AGA TGT 338

Fig. 11L

CCTTTGTAACCAAAATTTAGGTAAGCAGGCTTCCTTTGCTCTGAAGGTTTTGAGTACCTGGCTGTATTTTGTGAGTATT 1419
 TTTAAAAATTTTGGATAGTCTCTTAGGCAACAATAATCACAATATATTATCCCTTCAGTTCTGGAGAAAAGCCTGATACC 1498
 AGGCACAGCCTACTGACCCCAAGAGCCTGGCACTGATTGGCATCACATTTAGTCTAGAACTGTGTCCAGCCGCCGAAGAG 1577
 TAGGAAAAGAGAAGGCTGCTCAGGGAAACATTTGGCTGGGGCACGGAATAAGCACATAGTAAAAAGGGAACATCAGGG 1656
 TCAAAATGGAATCAACCTGAGACAGGAAACAGGGAGTTTCATTTGGCCACACTGGAAGAAAGGCAAGAAAGAGGAAACAA 1735
 GTCCTGGAGTACCCCTGGCTGTTCTCCACACTCACAAAGACATCAGCTATACTCTGCTTGTGCTAAGAAAGAGAAAAGA 1814
 GATGCCTTTTTGTGTTTGTAGTAAGAAATAATTAACCATAAGGAAGACCATGTATAAACTGATGGAAATAATAGTCACC 1893
 AAAGTACAGCACATACCATTTTGTGCTAATAACAATGTAGCACAGTAATGACTGTACATGTTCATTTGTATGTATACCAA 1972
 ACAAGATTGTTGTAATCATATTTTTTTATTACAACACTAAGTTCTGCTTCTGCAATTCCTAGGTTTCATCATTTTGGCT 2051
 CCTTAGCATGCCACTTACAATTTTTTAACATGAGATAACACATCAGGTGTGAGAACTTGCTTGAAGGGAATTACCAGA 2130
 AGTAATTTGTGTTTGAGATGGGGTGGAAATTGGAATTATATTAGTAGCCGGTGGAGATACAAAGTTCTCTGACTGTGTTG 2209
 GGAAGGATAAGTGCTACCGTTGAGAAAGGAGAAAGGCTGAGTCTAGGTGGAGAAAAATATCAACAGAACTCTAGCCA 2288
 AAGGCAAGCCCCAGAACTCAGACAAACAGAAAAGGAAATCCTAATCCTTCTGTTTTGAGAAAGAGAACTGTAGTTGCTTC 2367
 ACTTCCATTTTCATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACA 2446
 GTTTAAATTTCCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAAAGGAGCCCCAATGGCCTGGGTGGAGTGGGA 2525
 GTAGATAGGGAATATGTGGGATTGTGGTTTAAAGTTTCATCATTTGGGAGAGTTCCCTGGATCCTTGCAAGCTTAGATAAATGT 2604
 GATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAAAGGCAATGAAAATTTAGCAAGCCACTGAATTTGAGTTTTT 2683
 CACTTTGTTTCTAATATGCTGTGTAATCAGTACAGTTTCTTACCCCTTTCTTGGTCTTAATTTCCCTTACTGATAAAAT 2762
 GGGGTAGTAATACCTATCTCAAAAAATATTGCACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACAT 2841
 TAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAAGTAGCTTTTCAATTTGCTAGAAGCTTAAT 2920
 GTAGGCAAGCCACTTCATTTTTCAGAACTTGTCTACTCATTTATAATATGGGAATAAAAAATTTGTGCAAGTCAGAGAAG 2999
 GGTGCCTTAAAAATGTTGTGGCCAAGCCACATGAGATCAAGACACACTTTTCATGACCTCAAAATGTGGCCAGCCCTA 3078
 GGTGAGCCCAACCCCATCCAAACCTTAGACTCACGAAACAAATCCACCTGAGATCAGCAGAGCCACCTTAGATCAGCTGA 3157
 AACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAAAATAAAAAAGTCTCTCGTATAGCAAAATCTAA 3236

Fig. 11N

CTGATGCAATCTCCATCTGGCCTTCATCCTTCTCCCTTTATTGTGTCCTTTTCGTGTATTGTTCAATCCAGCAACCAGGATGA 3315
TCTTGTTAAACATTAACAGATTCTGTCAKCTTTMAAAAAAAAAAGCCATGAAATNTAGCAAGCCACTGAATTT 3394
GAGTTTTCACCTTTGTTTCTAATATGCTGTGTGAATCAGANCAGKTTTCTTACCCTTTCTTGGTCTTAATTTCTTACT 3473
GATAAAATGGGTGTAATACCTATCTCAAAAAATATTGCACATATTARATAACATTCCCTCTATGTATCTCAATGGCA 3552
TTAGACATTAGGAGAAGCATTTTGTGAGGATTTGAAGTTGAGATCTTCATCCAGAAAGTAGCTTTTCAATTTGSTAGA 3631
AGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTTGTTTACTCATTTATAATATGGGAATAAAAAATTTGTGCAAGT 3710
CAGAGAAGGTGTCCTTAAATAATGTTGTGGCCAGCCACATGAGATCAAGACACACTTTTCATGACCTCAAAATGTGGGC 3789
CCAGCCTAGGTCAGCCAAACCCCATCCAAACCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCTAGA 3868
TCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAATAAAAAAGAAAGACCTTGCCCCG 3947
GGCGGCGGCC 3958

Fig. 110

GAGACTGTGAAGAAGAAACGTTGCTTGGGCAAAAGAGCATATTCTCAGGAGACGGGGCCCTGCCTGCCACACCA 79
AGCATTAGGCCACCCAGGAAGACCCCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAGAGGCCCTGCAGCTCCTTC 158

M	N	W	H	M	I	I	S	G	L	I	V	V	V	L	K	V	V	G	19	
ATC	ATG	AAC	TGG	CAC	ATG	ATC	ATC	TCT	GGG	CTT	ATT	GTG	GTA	GTG	CTT	AAA	GTT	GTT	GGA	218
M	T	L	F	L	L	Y	F	C	P	K	D	W	E	F	Y	Q	A	R	C	39
ATG	ACC	TTA	TTT	CTA	CTT	TAT	TTC	TGC	CCC	AAA	GAC	TGG	GAA	TTT	TAT	CAA	GCA	AGA	TGT	278
F	F	L	S	T	S	E	S	S	W	N	E	S	R	D	F	C	K	G	K	59
TTT	TTC	TTA	TCC	ACT	TCT	GAA	TCA	TCT	TGG	AAT	GAA	AGC	AGG	GAC	TTT	TGC	AAA	GGA	AAA	338

Fig. 11P

G S T L A I V N T P E K L K F L Q D I T 79
GGA TCC ACA TTG GCA ATT GTC AAC ACG CCA GAG AAA CTG AAG TTT CTT CAG GAC ATA ACT 398

D A E K Y F I G L I Y H R E E K R W 99
GAT GCT GAG AAG TAT TTT ATT GGC TTA ATT TAC CAT CGT GAA GAG AAA AGG TGG CGT TGG 458

I N N S V F N G N V T N Q N F N C A 119
ATC AAC AAC TCT GTG TTC AAT GGC AAT GTT ACC AAT CAG AAT CAG AAT TTC AAC TGT GCG 518

T I G L T K T F D A A S C D I S Y R R I 139
ACC ATT GGC CTA ACA AAG ACA TTT GAT GCT GCA TCA TGT GAC ATC AGC TAC CGC AGG ATC 578

C E K N A K * 145
TGT GAG AAG AAT GCC AAA TGA 599

TCACAGTCCCTGTGACAAAGAACTATACCTTGCAACTCTTTTGAATCCATACAGGTCGTCTGGCCAATGATCTTTAC 678
TTACCTATCTGTCTACCAAGTAGCGGTCTTGCCCATTTGGGAAACTGAGCTTCTTTCTGCACTGGGGACTGGATG 757
CTAGCCATCTCAGGAGACAGGATCAGTTTACGGAAACAACACTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTAC 836
TGAGCATTTCTGACTGATCAAAAAGGCCCTAGTCTGTGACAGGGTTTGTATTTTAGCCTCAGAGTATACCATACATA 915
CTAGGGAGTAACTGTAGAGTGAGAAATATATAAACATTTATAGGGATTACCATGGTGGAAAGAGGATAAACATAGGTCC 994
TGTGACTTCGTCTGTCTCAAGGGAACCCCATTCACATGCCCCCTCCTAACTCCACAAGCAGGGTAGCAGAGGCTCT 1073
CCTCAGTCTGAACCTAAGGCTTGCCCTTGGGAGGGCTCCTAGTGTGAGCTTGGAGCAGCACGGACAGCAGCATTTGTTT 1152
ATGGGAATGGAGAGAGGTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAAACCAAGGAGCAAGGAGC 1231

Fig. 11Q

CAAACACACTAGATTCTGTCTTCAGCAAAAGCCCTGAAAGAGACACTTAAAGCTAAAAATTCCTTGTTCATATTTCTGAA
 1310
 ACTCCATTATAACATATGTAACCTCTTGTAAACCAAAATTTAGGTAAGCAGGCTTCCTTTGCTCTGAAGGTTTTGAGTA
 1389
 CCTGGCTGATTTTGTGAGTATTTTAAATTTTGGATAGTCTCTTAGGCAACAATAATCACAAATATATTCATCCCTTC
 1468
 AGTCTGGAGAAAGCCTGATACCAGGCACAGCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTGATCTA
 1547
 GAACTGTCCAGCCGCCGAGAGTAGGAAAAGAGAGGGCTGCTCAGGGAAACATTTGGCTGGGGCACGGAATAAGCAC
 1626
 ATAGTAAAAAGGGAACATCAGGGTCAATGGAAATCACCTGAGACAGGAAACAGGGAGTTTCATTTGGCCACACTGGAAG
 1705
 AAAGGCAAGAAAGAGGAAAGACAAGTCTTGGAGTACCCCTGGCTGTTCTCCACACTCACAAAGACATCAGCTATACTCTGCT
 1784
 TGGTGCAATAAGAAAGAGAAAGAGATGCCCTTTTGTGTTTGGTAAGAATAATTAAACCATAAGGAAGACCATGTATAA
 1863
 AACTGATGGAAATAATAGTCACCAAAAGTACAGCACATACCATTTTGTGTCTAATAACAATGTAGCACAGTAATGACTGT
 1942
 ACATGTCAATTGTATGTATACCAAAACAAGATTGTTGTAATCATATTTTATTATACAACACTAAAGTTCTGCTTCTGCATT
 2021
 CCTAGGTTTCATCATTTTGGCTCCTTAGCATGGCCACTTACAAATTTTAAACATGAGATAACACATCAGGTGTCAGAA
 2100
 CTTGCTTGAAGGGAATTACCAGAAAGTAATTTGTGTTTGGATGGGTGGAATTTGGAATTTATATAGTAGCCGGTGGAG
 2179
 ATACAAGTTCTCTGACTGTGTTGGGAAAGGATAAGTGCTACCGTTGAGAAAGGAAAGGCTGAGTCTAGGTGGAGAA
 2258
 AAATATCAACAGAACTCTAGCCAAAGGCAAGCCCAAGAACTCAGACAAACAGAAAGGAAATCCTAATCCTTCTGTTTGA
 2337
 GAAAGAGAACTGTAGTTGCTTCACCTTCCTATTTTCATGACAGAAATAACTGCAAACTTTTAAAGATCAGGAAATGTAGACA
 2416
 TCTAGTGATTTCTTTAGTAGACAGTTTAAATTTCCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCA
 2495
 ATGGCCTGGGTGGAGTGGGAGTAGATAGGGAATATGTGGATTTGGTTAAAGTTCATCATTTGGGAGAGTTCCCTGGA
 2574
 TCCCTGCAAGCTTAGATAAATGTGATCTTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAGGCAATGAAAAATTTA
 2653
 GCAAGCCACTGAATTTGAGTTTTCACCTTTGTTTCTAATATGCTGTGTGAATCAGTACAGTTTTTACCCCTTCTTGGT
 2732
 CTTAATTTCCCTTACTGATAAAATGGGGTAGTAATACCTATCTCAAAAATTTATTGCACATATTAAATAACATTCCTCTA
 2811
 TGTATCTCAATGGCATTAGACATTAGGAGAAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAGAAGTAGCT
 2890
 TTTCAATTTGCTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTATAATATGGAATA
 2969
 AAAATTTGTGCAAGTCAGAGAAGGGTGCCCTTAAAAATGTTGTGGCCAAAGCCACATGAGATCAAAGACACACTTTTTCATG
 3048
 ACCTCAAATGTGGGCCAGCCTAGGTGAGCCAAACCCCATCCAAACCTTAGACTCACGAACAAATCCACCTGAGATCAG
 3127

Fig. 11R

CAGAGCCACCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAAATAAAAAA 3206
 GTCTCTGTATAGCAAAATCTAACTGATGCAATCTCCATCTGGCCTTCATCCTTCTCCCTTTATTTGTCCTTTTCGTGTAT 3285
 TGTTCAATCCAGCAACCAGGATGATCTTTGTTAAACATTAACAGATTCTGTCA YKCTTMAAAAAAATAAAAAAGCCATGA 3364
 AATTNTAGCAAGCCACTGAAATTTGAGTTTTCACCTTTGGTTTCTAATATGCTGTGAAATCAGANCAGKTTTCTTACCCCT 3443
 TTCTTGGTCTTAATTTCCCTTACTGATAAAATGGGTWGTAAATACCTATCTCAAAAAATATTGCACATATTARATAACA 3522
 TTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAAGCATTTTGTGGAGGATTGGAAGTTGAGATCTTCATCCAAG 3601
 AAGTAGCTTTTCAATTTGSTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTATAATA 3680
 TGGGAATAAAAAATTTGTGCAAGTCAGAGAAGGTGCCCTTAAAAATGTTGTGCCAAGCCACATGAGATCAAGACACAC 3759
 TTTTCATGACCTCAAAATGTGGGCCAGCCTAGGTGAGCCAAACCCCATCCAACTTAGACTCACGAAACAAATCCACCT 3838
 GAGATCAGCAGAGCCACCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAA 3917
 AAAAAAA 3925

Fig. 11S

GAGACTGTGAAGAAGAAACGTTGCTTGGGCAAAAGGAGCATATTCTCAGGAGACGGGGCCCTGCCTGCCACACCA	79
AGCATTAGGCCACCAGGAAGACCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAGAGGCCCTGCAGCTCCTTC	158
M N W H M I I S G L I V V L K V V G	19
ATC ATG AAC TGG CAC ATG ATC ATC TCT GGG CTT ATT GTG GTA GTG CTT AAA GTT GTT GGA	218
M T L F L L Y F C P K D W E F Y Q A R C	39
ATG ACC TTA TTT CTA CTT TAT TTC TGC CCC AAA GAC TGG GAA TTT TAT CAA GCA AGA TGT	278
F F L S T S E S S W N E S R D F C K G K	59
TTT TTC TTA TCC ACT TCT GAA TCA TCT TGG AAT GAA AGC AGG GAC TTT TGC AAA GGA AAA	338
G S T L A I V N T P E K L K F L Q D I T	79
GGA TCC ACA TTG GCA ATT GTC AAC ACG CCA GAG AAA CTG AAG TTT CTT CAG GAC ATA ACT	398
D A E K Y F I G L I Y H R E E K R W R W	99
GAT GCT GAG AAG TAT TTT ATT GGC TTA ATT TAC CAT CGT GAA GAG AAA AGG TGG CGT TGG	458
I N N S V F N G K Y V N M P Q F P G D L	119
ATC AAC AAC TCT GTG TTC AAT GGC AAG TAC GTG AAC ATG CCA CAG TTT CCT GGG GAT CTT	518
G L L Q K T K P E I A G F T L E *	135
GGT TTG CTT CAA AAG ACC AAA CCT GAG ATT GCT GGG TTC ACC CTG GAA TAG	569

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Fig. 11T

CTCAAACGCTGACACTTGACTCTGTTCTGCTCTTCTCCTTTCTTCCAACCCATCTATTTCCCTATCTGTCTACCACTAGC 648
GGTCCCTTGCCCATTTGGGAAACTGAGCTTCTTTCTTGCACTGGGACTGGATGCTAGCCATCTCCAGGAGACAGGA 727
TCAGTTTACGGAAACAACTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTACTGAGCATTTCTGACTGATCAAAA 806
AGCCCTAGTCTGTTGACAGGGTTTGTTTATTTTAGCCTCAGAGTATACCATACTACTAGGAGTAACCTGTAGAGTGAG 885
AAATTATAAACATTATTTAGGGATTACCATGGTGGAAAGAGGGATAAACATAGGTCCTGTGACTTCGTCTCTGTCTCTCAA 964
GGAAACCCCATTCACATGCCCTCCTAACCTCCACAAGCGAGGTAGCAGAGGCTCTCCTCAGTCTGAACATAAGGCTTGG 1043
CCTTGGGGAGGGCTCCTAGTGTGAGCTTGAGCGACGACAGCAATTTGTTATGGGAATGGAGAGAGGTCTGGG 1122
CAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAAACCCAGGCAGCCAAAGGAGCCAAACACACTAGATTTCTGTCT 1201
TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCTTGTCTATATTTCTGAAACTCCATTTATAACATATGTAAC 1280
CCTTTGTAAACCAAAATTTAGGTAAGCAGGCTTCCCTTGTCTGAAGGTTTTGAGTACCTGGCTGTATTTGTTGAGTATT 1359
TTTAAAAATTTGGATAGTCTCTTAGGCAACAATAATCACAATATATTTCATCCCTTCAGTTCTGGAGAAAAGCCTGATACC 1438
AGGCACAGCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTGATCTAGAACTGGTCCAGCCGCCGAAGAG 1517
TAGGAAAAGAGAAAGGCTGCTCAGGGAAACATTGGCTGGGGCACGGAATAAGCACATAGTAAAAAGGGAACATCAGGG 1596
TCAAATGGAAATCACCTGAGACAGGAAACAGGGAGTTCAATTTGGCCACACTGGAAAGAAAGCAAGAGAAAGACAA 1675
GTCTTGGAGTACCCCTGGCTGTCTCCACACTCACAAGACATCAGCTATACTCTGCTTGGTGCATAAGAAAGAGAAAAGA 1754
GATGCCTTTTGTGTTTGTAGTAAGAAATAATTAACCATTAAGGAAGACCATGTATAAACTGATGGAATAATAGTCACC 1833
AAAGTACAGCACATACCAATTTGTGTCTAATAACAATGTAGCACAGTAATGACTGTACATGTCAATGTATGTATACCAA 1912
ACAAGATTGTTGTAAATCATATTTTATTACAACACTAAGTTCTGCTTCTGCATTCCTAGGTTTCATCATTTTGGCT 1991
CCTTAGCATGGCCACTTACAAATTTTAAACATGAGATAACACATCAGGTGTCAAGAACTTGCTTGAAGGGAATTACCCAGA 2070
AGTAATTTGTGTTTGTAGTGGGTGGAATTTGGAATTTATATTAGTAGCCGGTGGAGATACAAAGTTCTCTGACTGTGTG 2149
GGAAAGGATAAGTGCTACCGTTGAGAAAGGGAAGAAAGGCTGAGTCTAGGTGGAGAAAAATATCAACAGAACTCTAGCCA 2228
AAGGCAAGCCCCAGAACTCAGACAACAGAAAAGGAAATCCTAATCCTTCTGTTTGGAGAAAGAGAACTGTAGTTGCTTC 2307
ACTTCCATTTTCATGACAGAATAACTGCAAAATTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACA 2386

Fig. 11U

GTTTAATTTCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCAATGGCCCTGGGTGGAGTGGGGA 2465
GTAGATAGGGAATATGTGGGATTTGGTTAAGTTCATCATTTGGGAGAGTTCCTGGATCCTTGCAAGCTTAGATAAATGT 2544
GATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAAAGGCAATGAAAATTAGCAAGCCACTGAATTTGAGTTTT 2623
CACTTTGTTTCTAATATGCTGTGAATCAGTACAGTTTCTTACCCCTTTCTTGGTCTTAAATTTCCTTACTGATAAAAT 2702
GGGTAGTAATACCTATCTCAAAAAAATTATTGCACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACAT 2781
TAGGAGAAGCAATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAAGAAAGTAGCTTTTCAATTTGCTAGAAAGCTTAAT 2860
GTAGGCAAGCCACTTCATTTTCAGAACTTGTCTACTCATTTATAATATGGGAATAAAAATTTGTGCAAGTCAGAGAAG 2939
GGTGCCCTTAAAAATGTTGTGGCCAAGCCACATGAGATCAAAGACACACTTTTCATGACCTCAAATGTGGGCCAGCCTA 3018
GGTCAGCCAAACCCCATCCAAACCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGATCAGCTGA 3097
AACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAGTCTCTCGTATAGCAAAAATCTAA 3176
CTGATGCAATCTCCATCTGGCCCTTCATCCTTCTCCCTTTATTGTCTTTCGTGTAATGTTTCATCCAGCAACCAGGATGA 3255
TCTTGTAAAAACATTAAACAGATTCTGTCAKCTTMAAAAAAATAAAAAAGCCATGAAATNTAGCAAGCCACTGAATTT 3334
GAGTTTTCACCTTTGTTTCTAATATGCTGTGTGAATCAGANCAGKTTTCTTACCCCTTTCTTGGTCTTAAATTTCCCTTACT 3413
GATAAAATGGGTGTAAATACCTATCTCAAAAAAATTATTGCACATATTARATAACATTCCTCTATGTATCTCAATGGCA 3492
TTAGACATTAGGAGAAGCAATTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAAGAGTAGCTTTTCAATTTGSTAGA 3571
AGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTATAATATGGGAATAAAAAATTTGTGCAAGT 3650
CAGAGAAGGTGCCTTAAAAATGTTGTGGCCAAGCCACATGAGATCAAAGACACACTTTTCATGACCTCAAATGTGGGC 3729
CCAGCCTAGGTCAGCCAAACCCCATCCAAACCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGA 3808
TCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAGAAAGCACCTGCCCCG 3887
GGCGGCGGCCCC 3898

Fig. 11V

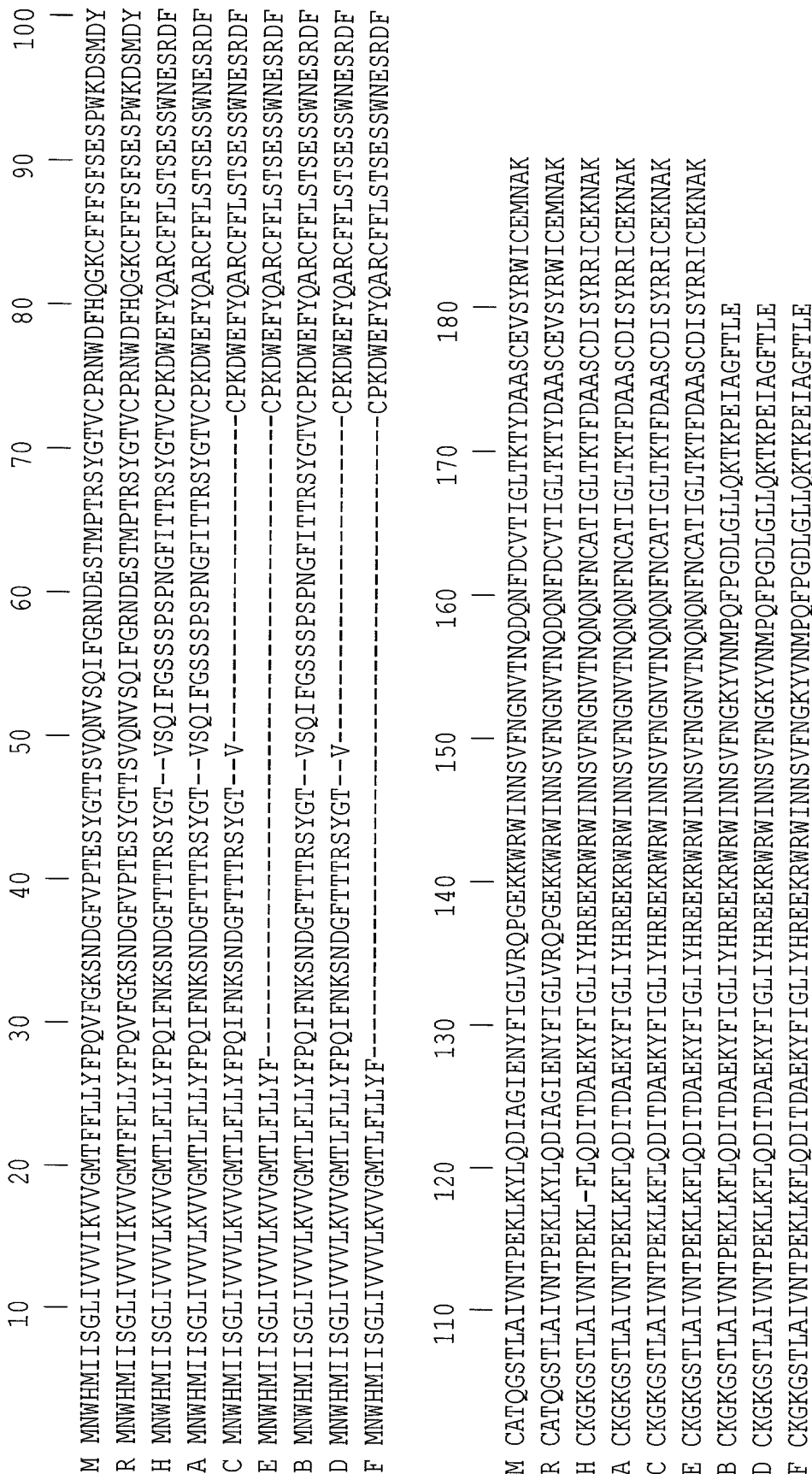


Fig. 11W

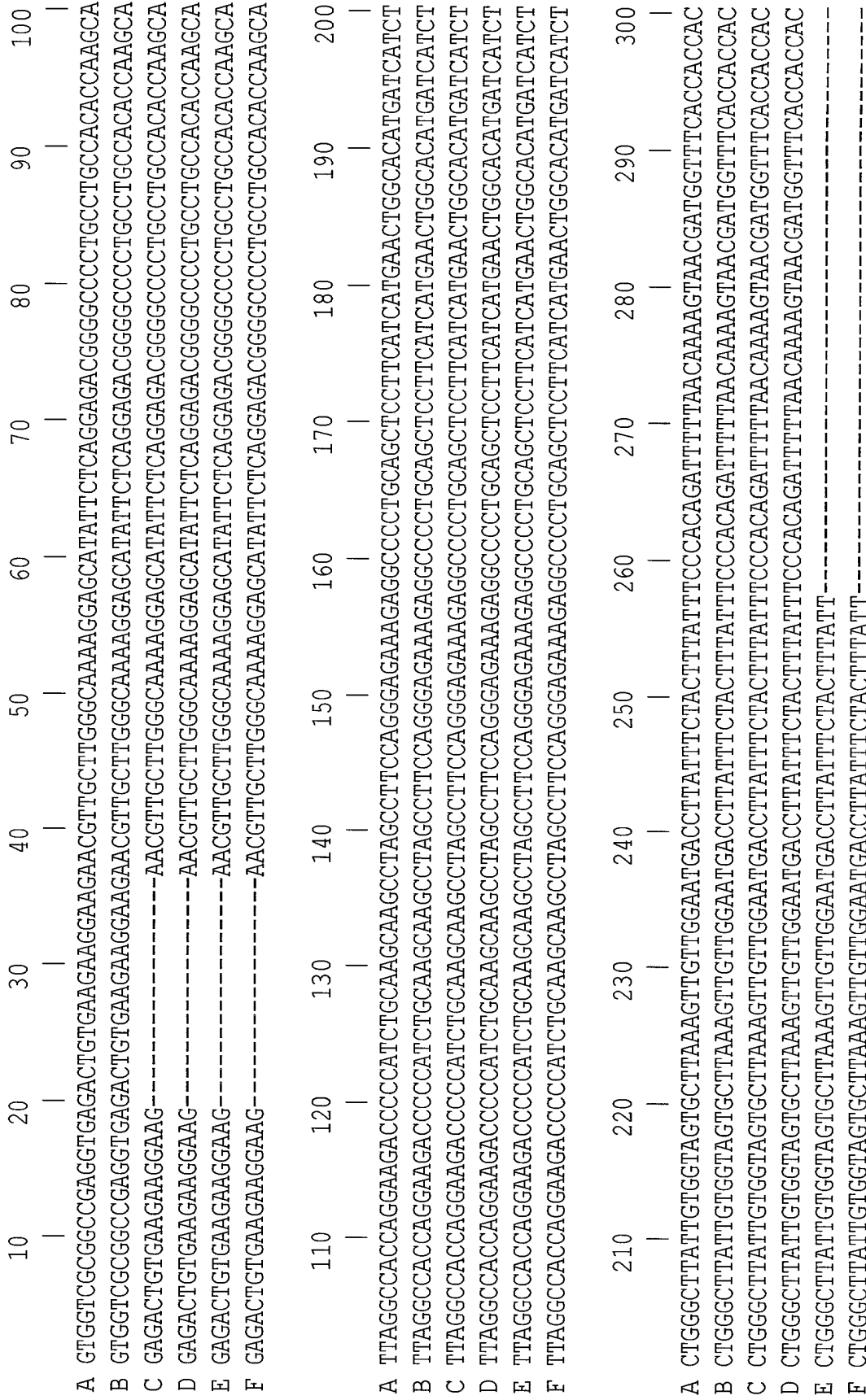


Fig. 11X-1

	310	320	330	340	350	360	370	380	390	400
A	CAGGAGCTATGGAACAGTCTCACAGATTTTGGGAGCAGTCCCAAGTCCCAACGGCTTCATTACCACAAGGAGCTATGGAACAGTCTGCCCCAAAGAC									
B	CAGGAGCTATGGAACAGTCTCACAGATTTTGGGAGCAGTCCCAAGTCCCAACGGCTTCATTACCACAAGGAGCTATGGAACAGTCTGCCCCAAAGAC									
C	CAGGAGCTATGGAACAG-----TCTGCCCCAAAGAC									
D	CAGGAGCTATGGAACAG-----TCTGCCCCAAAGAC									
E	-----TCTGCCCCAAAGAC									
F	-----TCTGCCCCAAAGAC									
	410	420	430	440	450	460	470	480	490	500
A	TGGGAATTTTATCAAGCAAGATGTTTTTCTTATCCACTTCTGAATCATCTTGAATGAAAGCAGGGACTTTTGCAAGGAAAAGGATCCACATTTGGCAA									
B	TGGGAATTTTATCAAGCAAGATGTTTTTCTTATCCACTTCTGAATCATCTTGAATGAAAGCAGGGACTTTTGCAAGGAAAAGGATCCACATTTGGCAA									
C	TGGGAATTTTATCAAGCAAGATGTTTTTCTTATCCACTTCTGAATCATCTTGAATGAAAGCAGGGACTTTTGCAAGGAAAAGGATCCACATTTGGCAA									
D	TGGGAATTTTATCAAGCAAGATGTTTTTCTTATCCACTTCTGAATCATCTTGAATGAAAGCAGGGACTTTTGCAAGGAAAAGGATCCACATTTGGCAA									
E	TGGGAATTTTATCAAGCAAGATGTTTTTCTTATCCACTTCTGAATCATCTTGAATGAAAGCAGGGACTTTTGCAAGGAAAAGGATCCACATTTGGCAA									
F	TGGGAATTTTATCAAGCAAGATGTTTTTCTTATCCACTTCTGAATCATCTTGAATGAAAGCAGGGACTTTTGCAAGGAAAAGGATCCACATTTGGCAA									
	510	520	530	540	550	560	570	580	590	600
A	TTGTCAACACGCCCAGAGAACTGAAGTTTCTTCAGGACATAAAGTATGCTGAGAAGTATTTTATTTGGCTTAATTTACCATCGTGAAGAGAAAAGGTGGCG									
B	TTGTCAACACGCCCAGAGAACTGAAGTTTCTTCAGGACATAAAGTATGCTGAGAAGTATTTTATTTGGCTTAATTTACCATCGTGAAGAGAAAAGGTGGCG									
C	TTGTCAACACGCCCAGAGAACTGAAGTTTCTTCAGGACATAAAGTATGCTGAGAAGTATTTTATTTGGCTTAATTTACCATCGTGAAGAGAAAAGGTGGCG									
D	TTGTCAACACGCCCAGAGAACTGAAGTTTCTTCAGGACATAAAGTATGCTGAGAAGTATTTTATTTGGCTTAATTTACCATCGTGAAGAGAAAAGGTGGCG									
E	TTGTCAACACGCCCAGAGAACTGAAGTTTCTTCAGGACATAAAGTATGCTGAGAAGTATTTTATTTGGCTTAATTTACCATCGTGAAGAGAAAAGGTGGCG									
F	TTGTCAACACGCCCAGAGAACTGAAGTTTCTTCAGGACATAAAGTATGCTGAGAAGTATTTTATTTGGCTTAATTTACCATCGTGAAGAGAAAAGGTGGCG									

Fig. 11X-2

	610	620	630	640	650	660	670	680	690	700
A	TTGGATCAACA	ACTCTGTGTTCA	ATGGCAATGTTACCA	ATCAGAATCAGA	ATTTCAACTGTGCG	ACCATTGGCC	TAAACAAGAC	ATTTGATGCTGC	ATCA	
B	TTGGATCAACA	ACTCTGTGTTCA	ATGGCAAGTACGTGA	ACATGCCACAGTTT	CCTGGGATCTTGG	TTGCTTCAAA	AGACCAACCT	GAGATTGCT	TGGG	
C	TTGGATCAACA	ACTCTGTGTTCA	ATGGCAATGTTACCA	ATCAGAATCAGA	ATTTCAACTGTGCG	ACCATTGGCC	TAAACAAGAC	ATTTGATGCTGC	ATCA	
D	TTGGATCAACA	ACTCTGTGTTCA	ATGGCAAGTACGTGA	ACATGCCACAGTTT	CCTGGGATCTTGG	TTGCTTCAAA	AGACCAACCT	GAGATTGCT	TGGG	
E	TTGGATCAACA	ACTCTGTGTTCA	ATGGCAATGTTACCA	ATCAGAATCAGA	ATTTCAACTGTGCG	ACCATTGGCC	TAAACAAGAC	ATTTGATGCTGC	ATCA	
F	TTGGATCAACA	ACTCTGTGTTCA	ATGGCAAGTACGTGA	ACATGCCACAGTTT	CCTGGGATCTTGG	TTGCTTCAAA	AGACCAACCT	GAGATTGCT	TGGG	
	710	720	730	740	750	760	770	780	790	800
A	TGTGACATCAG	TACCGCAGGAT	CTGTGAGAAGAA	TGCCAAATGATC	ACAGTCCCTGTG	ACAAGAACTAT	ACTTGCAACT	CTTTTGAAT	CCATACAGG	
B	TTACCCCTGGA	ATAGCTCAAA	CGTGACACTT	GACTCTGTTCT	CTTCTCCCTT	CTTCCAACCC	ATCTATTTC	-----		
C	TGTGACATCAG	TACCGCAGGAT	CTGTGAGAAGAA	TGCCAAATGATC	ACAGTCCCTGTG	ACAAGAACTAT	ACTTGCAACT	CTTTTGAAT	CCATACAGG	
D	TTACCCCTGGA	ATAGCTCAAA	CGTGACACTT	GACTCTGTTCT	CTTCTCCCTT	CTTCCAACCC	ATCTATTTC	-----		
E	TGTGACATCAG	TACCGCAGGAT	CTGTGAGAAGAA	TGCCAAATGATC	ACAGTCCCTGTG	ACAAGAACTAT	ACTTGCAACT	CTTTTGAAT	CCATACAGG	
F	TTACCCCTGGA	ATAGCTCAAA	CGTGACACTT	GACTCTGTTCT	CTTCTCCCTT	CTTCCAACCC	ATCTATTTC	-----		
	810	820	830	840	850	860	870	880	890	900
A	TCGCTGGCCAA	TGATTTTACTT	ACCTATCTGTCT	ACCAGTAGCGG	TCCCTTGCCCA	TTTGGGAAACT	GAGCTTCTTT	CTGCACTGGG	GACTGG	
B	-----									
C	TCGCTGGCCAA	TGATTTTACTT	ACCTATCTGTCT	ACCAGTAGCGG	TCCCTTGCCCA	TTTGGGAAACT	GAGCTTCTTT	CTGCACTGGG	GACTGG	
D	-----									
E	TCGCTGGCCAA	TGATTTTACTT	ACCTATCTGTCT	ACCAGTAGCGG	TCCCTTGCCCA	TTTGGGAAACT	GAGCTTCTTT	CTGCACTGGG	GACTGG	
F	-----									

Fig. 11X-3

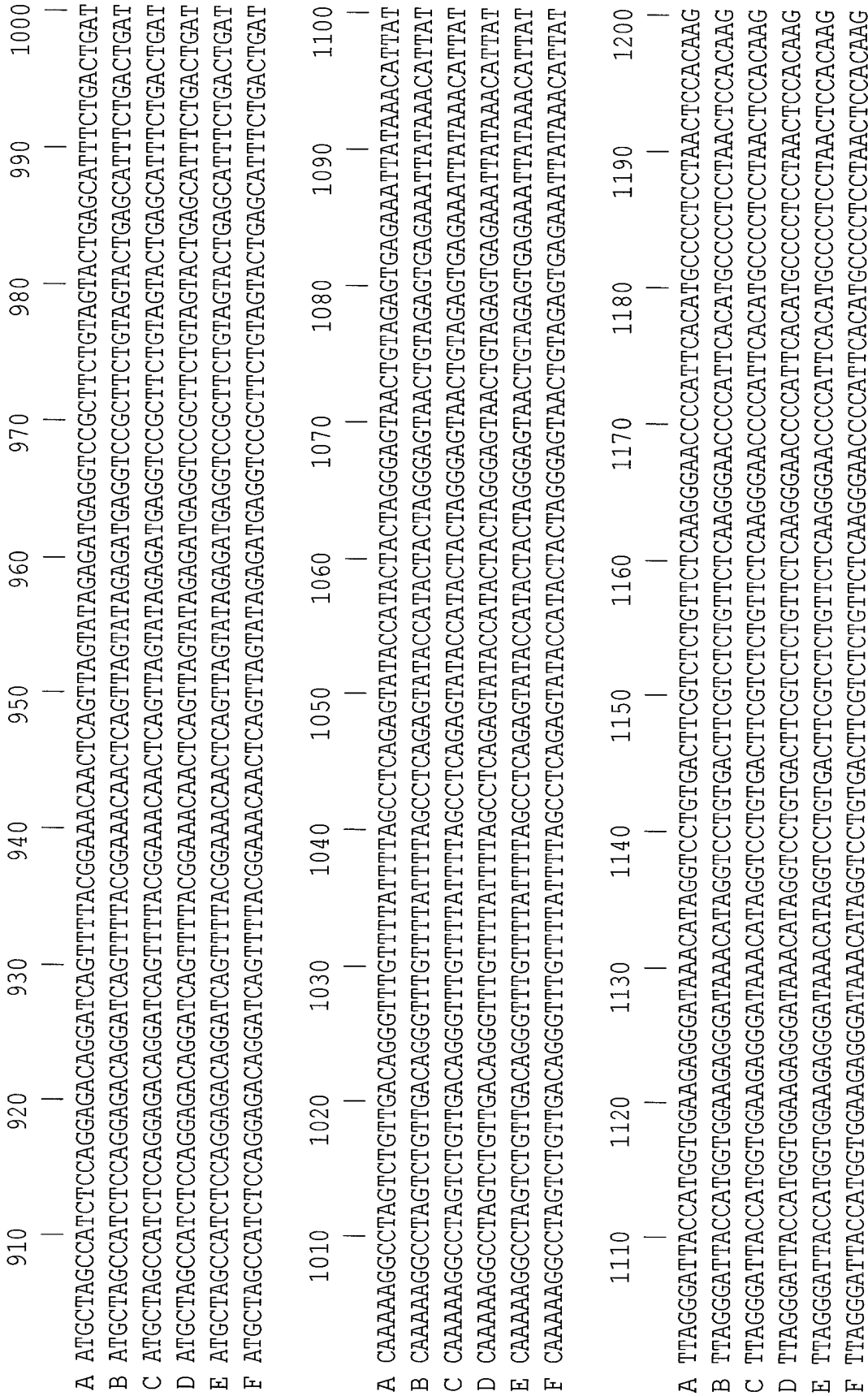


Fig. 11X-4

1210		1220		1230		1240		1250		1260		1270		1280		1290		1300
A	CGAGGGTAGCAGAGGCTCTCCCTCAGTCTGAACCTAAGGCTTGGCCCTTGGGAGGGCTCCTAGTGTGAGCTTGGAGCAGCAGGACAGCAGCATTGTTTAT																	
B	CGAGGGTAGCAGAGGCTCTCCCTCAGTCTGAACCTAAGGCTTGGCCCTTGGGAGGGCTCCTAGTGTGAGCTTGGAGCAGCAGGACAGCAGCATTGTTTAT																	
C	CGAGGGTAGCAGAGGCTCTCCCTCAGTCTGAACCTAAGGCTTGGCCCTTGGGAGGGCTCCTAGTGTGAGCTTGGAGCAGCAGGACAGCAGCATTGTTTAT																	
D	CGAGGGTAGCAGAGGCTCTCCCTCAGTCTGAACCTAAGGCTTGGCCCTTGGGAGGGCTCCTAGTGTGAGCTTGGAGCAGCAGGACAGCAGCATTGTTTAT																	
E	CGAGGGTAGCAGAGGCTCTCCCTCAGTCTGAACCTAAGGCTTGGCCCTTGGGAGGGCTCCTAGTGTGAGCTTGGAGCAGCAGGACAGCAGCATTGTTTAT																	
F	CGAGGGTAGCAGAGGCTCTCCCTCAGTCTGAACCTAAGGCTTGGCCCTTGGGAGGGCTCCTAGTGTGAGCTTGGAGCAGCAGGACAGCAGCATTGTTTAT																	
1310		1320		1330		1340		1350		1360		1370		1380		1390		1400
A	GGGAATGGAGAGAGGTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTGAAGAAAAACCAGGCAGCCAAAGGAGGCCAAAACACACTAGATTTCGTCTCT																	
B	GGGAATGGAGAGAGGTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTGAAGAAAAACCAGGCAGCCAAAGGAGCCAAAACACACTAGATTTCGTCTCT																	
C	GGGAATGGAGAGAGGTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTGAAGAAAAACCAGGCAGCCAAAGGAGGCCAAAACACACTAGATTTCGTCTCT																	
D	GGGAATGGAGAGAGGTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTGAAGAAAAACCAGGCAGCCAAAGGAGGCCAAAACACACTAGATTTCGTCTCT																	
E	GGGAATGGAGAGAGGTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTGAAGAAAAACCAGGCAGCCAAAGGAGGCCAAAACACACTAGATTTCGTCTCT																	
F	GGGAATGGAGAGAGGTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTGAAGAAAAACCAGGCAGCCAAAGGAGGCCAAAACACACTAGATTTCGTCTCT																	
1410		1420		1430		1440		1450		1460		1470		1480		1490		1500
A	TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCTTGTCAATTTCTGAAACTCCATTATAACATATGTAACCTCCTTTGTAACCCAAAAATTAGG																	
B	TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCTTGTCAATTTCTGAAACTCCATTATAACATATGTAACCTCCTTTGTAACCCAAAAATTAGG																	
C	TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCTTGTCAATTTCTGAAACTCCATTATAACATATGTAACCTCCTTTGTAACCCAAAAATTAGG																	
D	TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCTTGTCAATTTCTGAAACTCCATTATAACATATGTAACCTCCTTTGTAACCCAAAAATTAGG																	
E	TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCTTGTCAATTTCTGAAACTCCATTATAACATATGTAACCTCCTTTGTAACCCAAAAATTAGG																	
F	TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCTTGTCAATTTCTGAAACTCCATTATAACATATGTAACCTCCTTTGTAACCCAAAAATTAGG																	

Fig. 11X-5

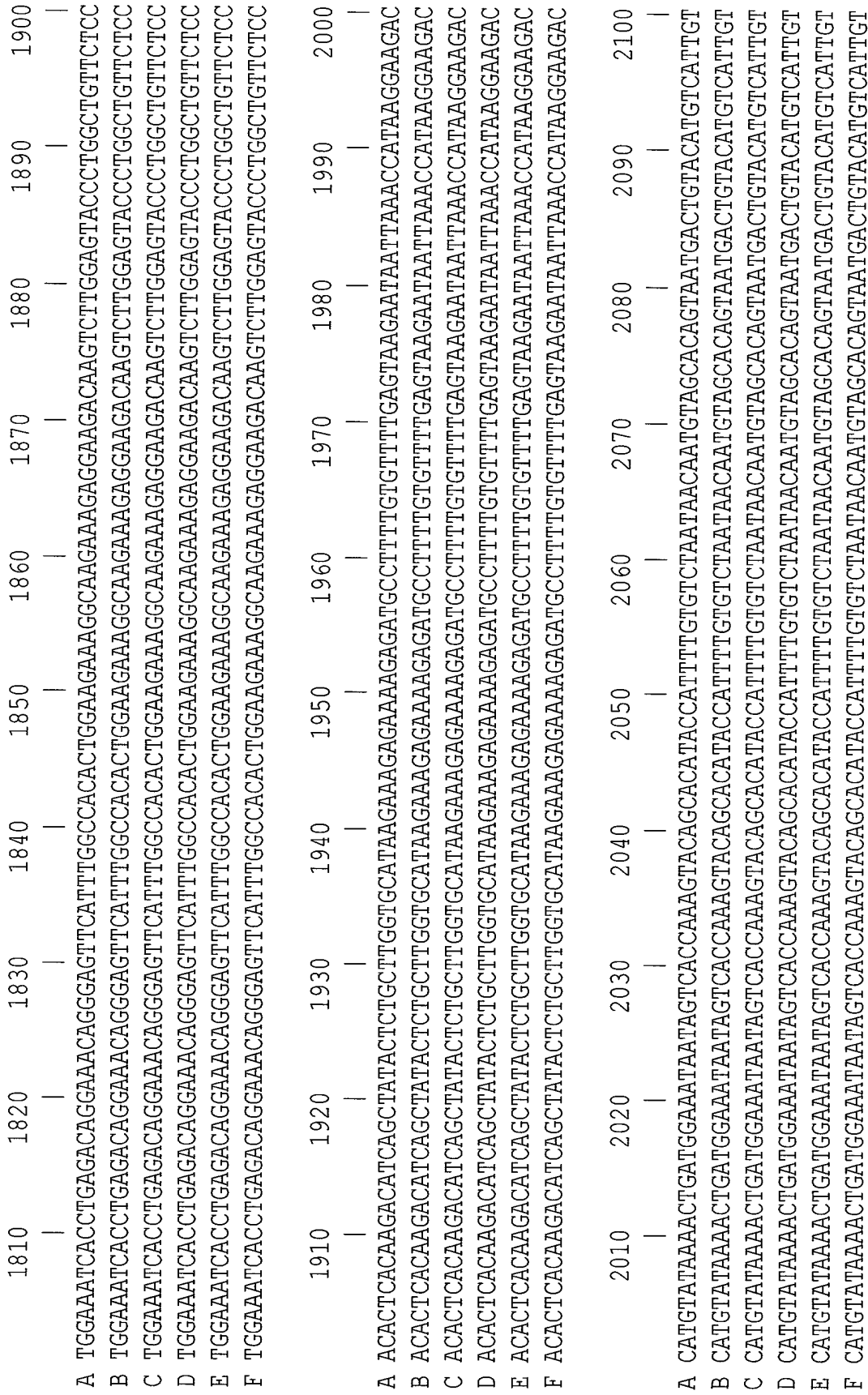


Fig. 11X-7

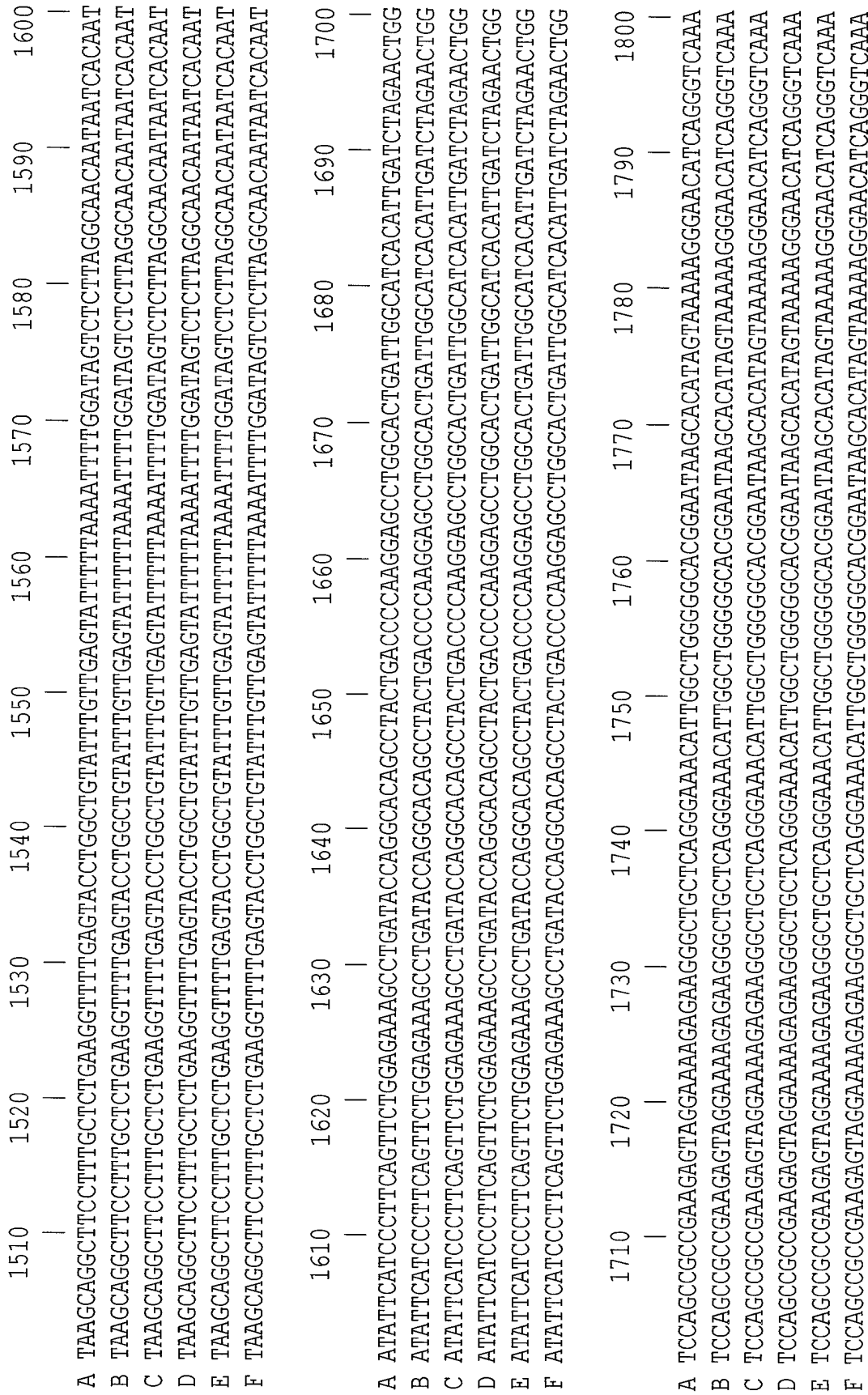


Fig. 11X-6

2110	2120	2130	2140	2150	2160	2170	2180	2190	2200
A	ATGTATACCAACAAGATTGTTGTAAATCATATTTTATTACAACACTAAGTCTGCTTCTGCATTCCTAGGTTTCATCATTTTGGCTCCTTAGCATG								
B	ATGTATACCAACAAGATTGTTGTAAATCATATTTTATTACAACACTAAGTCTGCTTCTGCATTCCTAGGTTTCATCATTTTGGCTCCTTAGCATG								
C	ATGTATACCAACAAGATTGTTGTAAATCATATTTTATTACAACACTAAGTCTGCTTCTGCATTCCTAGGTTTCATCATTTTGGCTCCTTAGCATG								
D	ATGTATACCAACAAGATTGTTGTAAATCATATTTTATTACAACACTAAGTCTGCTTCTGCATTCCTAGGTTTCATCATTTTGGCTCCTTAGCATG								
E	ATGTATACCAACAAGATTGTTGTAAATCATATTTTATTACAACACTAAGTCTGCTTCTGCATTCCTAGGTTTCATCATTTTGGCTCCTTAGCATG								
F	ATGTATACCAACAAGATTGTTGTAAATCATATTTTATTACAACACTAAGTCTGCTTCTGCATTCCTAGGTTTCATCATTTTGGCTCCTTAGCATG								
2210	2220	2230	2240	2250	2260	2270	2280	2290	2300
A	GCCACTTACAAATTTTAAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGAAGTAATTTGTGTTGAGATGGGGTGGAAATT								
B	GCCACTTACAAATTTTAAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGAAGTAATTTGTGTTGAGATGGGGTGGAAATT								
C	GCCACTTACAAATTTTAAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGAAGTAATTTGTGTTGAGATGGGGTGGAAATT								
D	GCCACTTACAAATTTTAAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGAAGTAATTTGTGTTGAGATGGGGTGGAAATT								
E	GCCACTTACAAATTTTAAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGAAGTAATTTGTGTTGAGATGGGGTGGAAATT								
F	GCCACTTACAAATTTTAAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGAAGTAATTTGTGTTGAGATGGGGTGGAAATT								
2310	2320	2330	2340	2350	2360	2370	2380	2390	2400
A	GGAATTATATTAGTAGCCGGTGGAGATACAAAGTTCTCTGACTGTGTTGGGAAAGGATAAGTGTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGG								
B	GGAATTATATTAGTAGCCGGTGGAGATACAAAGTTCTCTGACTGTGTTGGGAAAGGATAAGTGTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGG								
C	GGAATTATATTAGTAGCCGGTGGAGATACAAAGTTCTCTGACTGTGTTGGGAAAGGATAAGTGTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGG								
D	GGAATTATATTAGTAGCCGGTGGAGATACAAAGTTCTCTGACTGTGTTGGGAAAGGATAAGTGTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGG								
E	GGAATTATATTAGTAGCCGGTGGAGATACAAAGTTCTCTGACTGTGTTGGGAAAGGATAAGTGTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGG								
F	GGAATTATATTAGTAGCCGGTGGAGATACAAAGTTCTCTGACTGTGTTGGGAAAGGATAAGTGTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGG								

Fig. 11X-8

Figure 11X-9

2410	2420	2430	2440	2450	2460	2470	2480	2490	2500
A	AGAAAAATATCAACAGAACTCTAGCCAAAGGCAAGCCCCAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTTGAGAAAGAGAGAACTGTAGT								
B	AGAAAAATATCAACAGAACTCTAGCCAAAGGCAAGCCCCAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTTGAGAAAGAGAGAACTGTAGT								
C	AGAAAAATATCAACAGAACTCTAGCCAAAGGCAAGCCCCAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTTGAGAAAGAGAGAACTGTAGT								
D	AGAAAAATATCAACAGAACTCTAGCCAAAGGCAAGCCCCAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTTGAGAAAGAGAGAACTGTAGT								
E	AGAAAAATATCAACAGAACTCTAGCCAAAGGCAAGCCCCAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTTGAGAAAGAGAGAACTGTAGT								
F	AGAAAAATATCAACAGAACTCTAGCCAAAGGCAAGCCCCAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTTGAGAAAGAGAGAACTGTAGT								
2510	2520	2530	2540	2550	2560	2570	2580	2590	2600
A	TGCTTCACTTCCTATTTTCATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACAGTTTAATTTCCCCCA								
B	TGCTTCACTTCCTATTTTCATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACAGTTTAATTTCCCCCA								
C	TGCTTCACTTCCTATTTTCATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACAGTTTAATTTCCCCCA								
D	TGCTTCACTTCCTATTTTCATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACAGTTTAATTTCCCCCA								
E	TGCTTCACTTCCTATTTTCATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACAGTTTAATTTCCCCCA								
F	TGCTTCACTTCCTATTTTCATGACAGAAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACAGTTTAATTTCCCCCA								
2610	2620	2630	2640	2650	2660	2670	2680	2690	2700
A	AGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGGTGGGAGTGGGGAGTAGATAGGGAATATGTGGGATTTGGTTAAGTTCA								
B	AGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGGTGGGAGTGGGGAGTAGATAGGGAATATGTGGGATTTGGTTAAGTTCA								
C	AGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGGTGGGAGTGGGGAGTAGATAGGGAATATGTGGGATTTGGTTAAGTTCA								
D	AGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGGTGGGAGTGGGGAGTAGATAGGGAATATGTGGGATTTGGTTAAGTTCA								
E	AGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGGTGGGAGTGGGGAGTAGATAGGGAATATGTGGGATTTGGTTAAGTTCA								
F	AGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGGTGGGAGTGGGGAGTAGATAGGGAATATGTGGGATTTGGTTAAGTTCA								

Fig. 11X-9

Figure 11X-10

2710	2720	2730	2740	2750	2760	2770	2780	2790	2800
A	TCATTGGGAGAGTTCCTGGATCCTTGCAAGCTTAGATAAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAGGCAATGAAAAATTAG								
B	TCATTGGGAGAGTTCCTGGATCCTTGCAAGCTTAGATAAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAGGCAATGAAAAATTAG								
C	TCATTGGGAGAGTTCCTGGATCCTTGCAAGCTTAGATAAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAGGCAATGAAAAATTAG								
D	TCATTGGGAGAGTTCCTGGATCCTTGCAAGCTTAGATAAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAGGCAATGAAAAATTAG								
E	TCATTGGGAGAGTTCCTGGATCCTTGCAAGCTTAGATAAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAGGCAATGAAAAATTAG								
F	TCATTGGGAGAGTTCCTGGATCCTTGCAAGCTTAGATAAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAGGCAATGAAAAATTAG								
2810	2820	2830	2840	2850	2860	2870	2880	2890	2900
A	CAAGCCACTGAATTTGAGTTTTTCACTTTGTTTCTAAATGCTGTGTAATCAGTACAGTTTTCTTACCCTTTCTTGGTCTTAATTTCCTTACTGATAAAA								
B	CAAGCCACTGAATTTGAGTTTTTCACTTTGTTTCTAAATGCTGTGTAATCAGTACAGTTTTCTTACCCTTTCTTGGTCTTAATTTCCTTACTGATAAAA								
C	CAAGCCACTGAATTTGAGTTTTTCACTTTGTTTCTAAATGCTGTGTAATCAGTACAGTTTTCTTACCCTTTCTTGGTCTTAATTTCCTTACTGATAAAA								
D	CAAGCCACTGAATTTGAGTTTTTCACTTTGTTTCTAAATGCTGTGTAATCAGTACAGTTTTCTTACCCTTTCTTGGTCTTAATTTCCTTACTGATAAAA								
E	CAAGCCACTGAATTTGAGTTTTTCACTTTGTTTCTAAATGCTGTGTAATCAGTACAGTTTTCTTACCCTTTCTTGGTCTTAATTTCCTTACTGATAAAA								
F	CAAGCCACTGAATTTGAGTTTTTCACTTTGTTTCTAAATGCTGTGTAATCAGTACAGTTTTCTTACCCTTTCTTGGTCTTAATTTCCTTACTGATAAAA								
2910	2920	2930	2940	2950	2960	2970	2980	2990	3000
A	TGGGGTAGTAACCTATCTCAAAAAAATTATTGCACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGA								
B	TGGGGTAGTAACCTATCTCAAAAAAATTATTGCACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGA								
C	TGGGGTAGTAACCTATCTCAAAAAAATTATTGCACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGA								
D	TGGGGTAGTAACCTATCTCAAAAAAATTATTGCACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGA								
E	TGGGGTAGTAACCTATCTCAAAAAAATTATTGCACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGA								
F	TGGGGTAGTAACCTATCTCAAAAAAATTATTGCACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGA								

Fig. 11X-10

	3010	3020	3030	3040	3050	3060	3070	3080	3090	3100
A	GGATTGAAGTTGAGATCTTCA	TCCAAGAAGTAGCTTTTCA	ATTGCTAGAAAGCTTAAT	GTAGGCAAGCCACTTCAT	TTTTCAGAACTTGT	TACTCATT				
B	GGATTGAAGTTGAGATCTTCA	TCCAAGAAGTAGCTTTTCA	ATTGCTAGAAAGCTTAAT	GTAGGCAAGCCACTTCAT	TTTTCAGAACTTGT	TACTCATT				
C	GGATTGAAGTTGAGATCTTCA	TCCAAGAAGTAGCTTTTCA	ATTGCTAGAAAGCTTAAT	GTAGGCAAGCCACTTCAT	TTTTCAGAACTTGT	TACTCATT				
D	GGATTGAAGTTGAGATCTTCA	TCCAAGAAGTAGCTTTTCA	ATTGCTAGAAAGCTTAAT	GTAGGCAAGCCACTTCAT	TTTTCAGAACTTGT	TACTCATT				
E	GGATTGAAGTTGAGATCTTCA	TCCAAGAAGTAGCTTTTCA	ATTGCTAGAAAGCTTAAT	GTAGGCAAGCCACTTCAT	TTTTCAGAACTTGT	TACTCATT				
F	GGATTGAAGTTGAGATCTTCA	TCCAAGAAGTAGCTTTTCA	ATTGCTAGAAAGCTTAAT	GTAGGCAAGCCACTTCAT	TTTTCAGAACTTGT	TACTCATT				
	3110	3120	3130	3140	3150	3160	3170	3180	3190	3200
A	TATAATATGGGAATAAAAA	TTTGTGCAAGTCAGAGAAGGGTG	CCCTTAAAAATGTTGTG	CCCAAGCCACATGAGAT	CAAAAGACACACTTTT	CATGACCTCA				
B	TATAATATGGGAATAAAAA	TTTGTGCAAGTCAGAGAAGGGTG	CCCTTAAAAATGTTGTG	CCCAAGCCACATGAGAT	CAAAAGACACACTTTT	CATGACCTCA				
C	TATAATATGGGAATAAAAA	TTTGTGCAAGTCAGAGAAGGGTG	CCCTTAAAAATGTTGTG	CCCAAGCCACATGAGAT	CAAAAGACACACTTTT	CATGACCTCA				
D	TATAATATGGGAATAAAAA	TTTGTGCAAGTCAGAGAAGGGTG	CCCTTAAAAATGTTGTG	CCCAAGCCACATGAGAT	CAAAAGACACACTTTT	CATGACCTCA				
E	TATAATATGGGAATAAAAA	TTTGTGCAAGTCAGAGAAGGGTG	CCCTTAAAAATGTTGTG	CCCAAGCCACATGAGAT	CAAAAGACACACTTTT	CATGACCTCA				
F	TATAATATGGGAATAAAAA	TTTGTGCAAGTCAGAGAAGGGTG	CCCTTAAAAATGTTGTG	CCCAAGCCACATGAGAT	CAAAAGACACACTTTT	CATGACCTCA				
	3210	3220	3230	3240	3250	3260	3270	3280	3290	3300
A	AATGTGGCCCGAGCCTAGGT	CAGCCAAACCCCATCCA	ACCCCTTAGACTCAGCA	ACAAATCCACCTGAGAT	CAGCAGAGCCACCC	CTAGATCAGCTGAA	AACT			
B	AATGTGGCCCGAGCCTAGGT	CAGCCAAACCCCATCCA	ACCCCTTAGACTCAGCA	ACAAATCCACCTGAGAT	CAGCAGAGCCACCC	CTAGATCAGCTGAA	AACT			
C	AATGTGGCCCGAGCCTAGGT	CAGCCAAACCCCATCCA	ACCCCTTAGACTCAGCA	ACAAATCCACCTGAGAT	CAGCAGAGCCACCC	CTAGATCAGCTGAA	AACT			
D	AATGTGGCCCGAGCCTAGGT	CAGCCAAACCCCATCCA	ACCCCTTAGACTCAGCA	ACAAATCCACCTGAGAT	CAGCAGAGCCACCC	CTAGATCAGCTGAA	AACT			
E	AATGTGGCCCGAGCCTAGGT	CAGCCAAACCCCATCCA	ACCCCTTAGACTCAGCA	ACAAATCCACCTGAGAT	CAGCAGAGCCACCC	CTAGATCAGCTGAA	AACT			
F	AATGTGGCCCGAGCCTAGGT	CAGCCAAACCCCATCCA	ACCCCTTAGACTCAGCA	ACAAATCCACCTGAGAT	CAGCAGAGCCACCC	CTAGATCAGCTGAA	AACT			

Fig. 11X-11

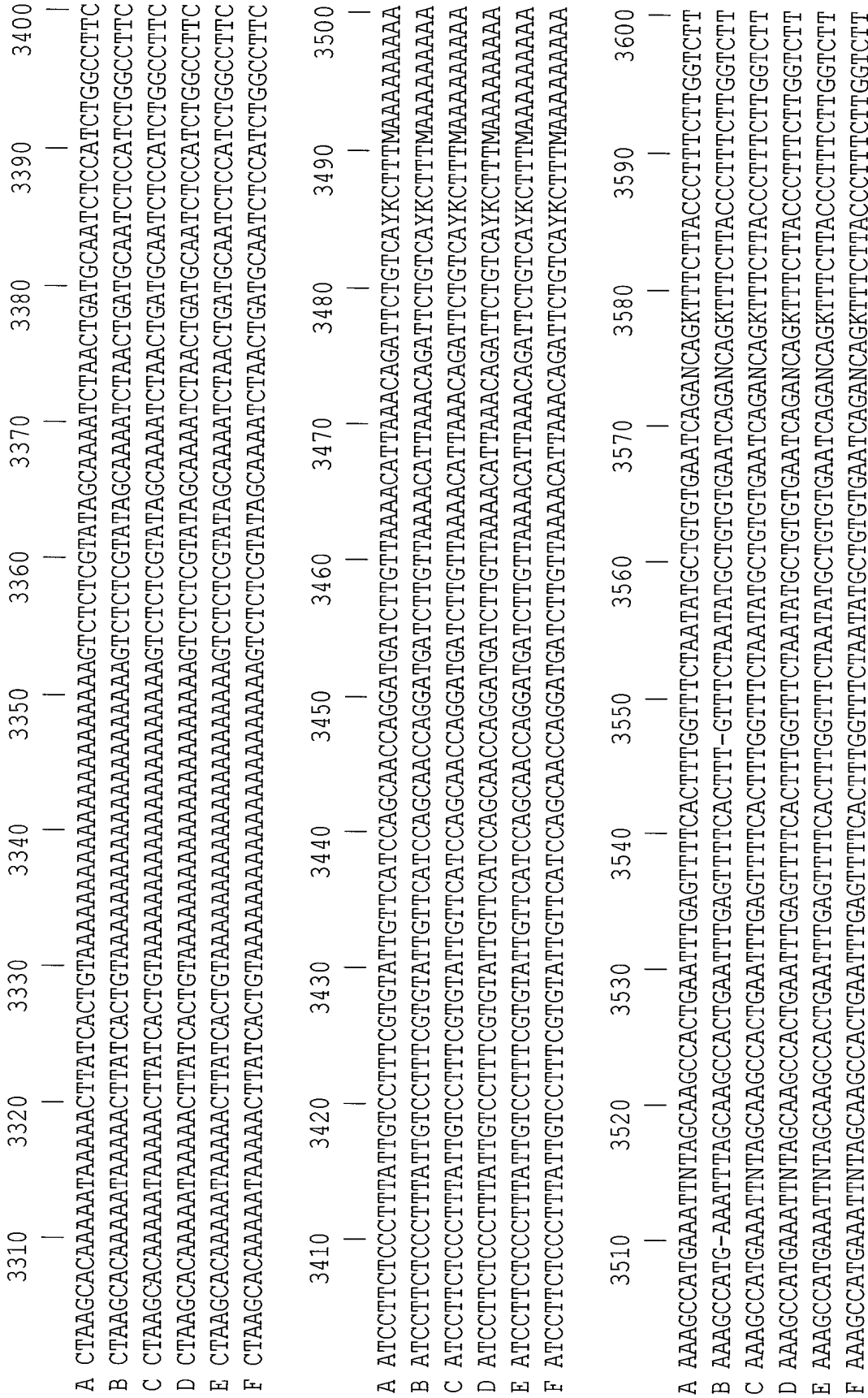


Fig. 11X-12

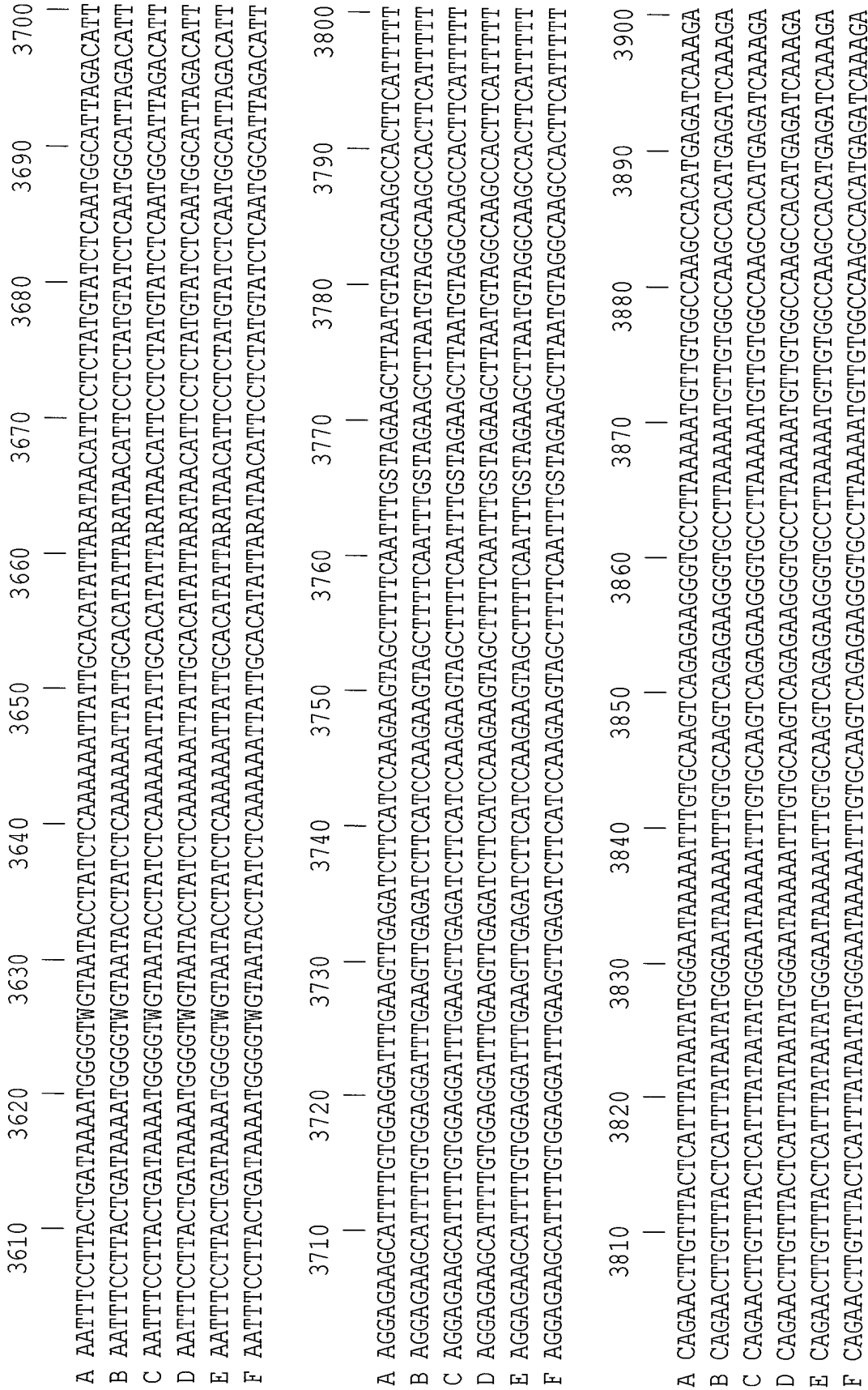


Fig. 11X-13

4010	4020	4030	4040	4050	4060	4070	4080	4090
------	------	------	------	------	------	------	------	------

A CCC TAGAT CAGCT GAAACTCTAAGCACAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAAAAAAAAAAAAGAACACCTGCCCGGGCGGGCGCCCC
 B CCC TAGAT CAGCT GAAACTCTAAGCACAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAAAAAAAAAAAAGAACACCTGCCCGGGCGGGCGCCCC
 C CCC TAGAT CAGCT GAAACTCTAAGCACAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAAAAAAAAAAAAGAACACCTGCCCGGGCGGGCGCCCC
 D CCC TAGAT CAGCT GAAACTCTAAGCACAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAAAAAAAAAAAAGAACACCTGCCCGGGCGGGCGCCCC
 E CCC TAGAT CAGCT GAAACTCTAAGCACAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAAAAAAAAAAAAGAACACCTGCCCGGGCGGGCGCCCC
 F CCC TAGAT CAGCT GAAACTCTAAGCACAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAAAAAAAAAAAAGAACACCTGCCCGGGCGGGCGGGCGCCCC

Fig. 11X-14

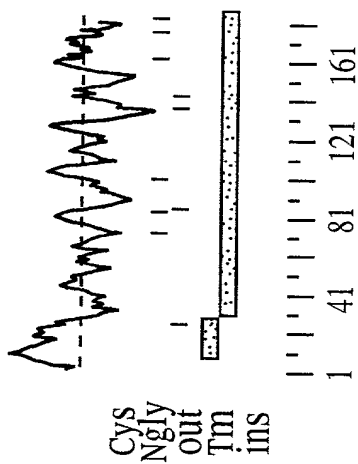


FIG. 11Y-1

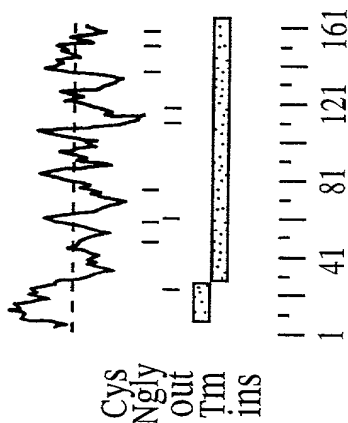


FIG. 11Y-3

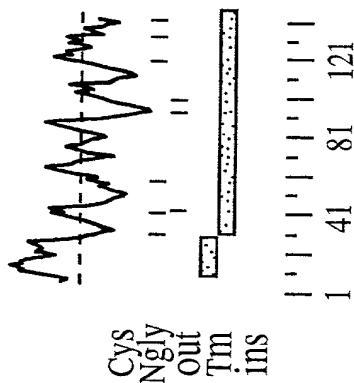


FIG. 11Y-5

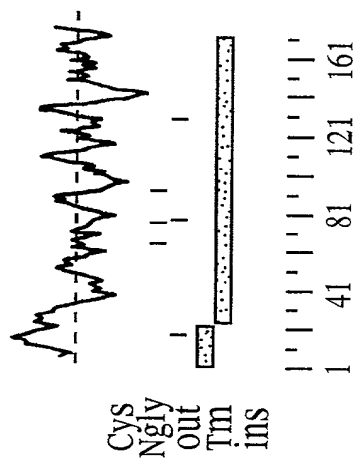


FIG. 11Y-2

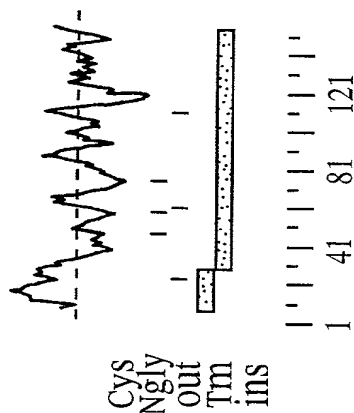


FIG. 11Y-4

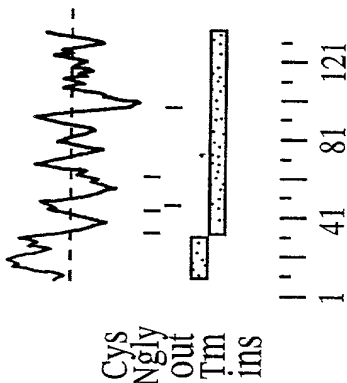


FIG. 11Y-6

GTCGACCCAC	GCGTCCGGTT	TGCTTGAGA	TGCTGTAAA	ACAGAGAGGC	TGTGAACAAG
GACATTACC	AGCAGGAGCA	TACATTCAGA	AGACAAGGAG	CCCTGCTCGC	TGCACCCGAAT
ATCTTATCAA	AAAGACTCCT	ATCTGTATGC	CAACCCAGAC	TTCCAGAAAG	AGATCAGATC
CCTGAATCCC	CATCATC	ATG AAC TGG CAC ATG ATC ATC TCG GGG CTT ATC			
	Met Asn Trp His Met Ile Ile Ser Gly Leu Ile				
	1	5	10		
GTA GTA GTG ATC AAA GTT GTT GGA ATG ACC TTT TTT CTG CTC TAT TTC					
Val Val Val Ile Lys Val Val Gly Met Thr Phe Phe Leu Leu Tyr Phe					
	15	20	25		
CCA CAG GTT TTT GGC AAA AGT AAT GAT GGC TTC GTC CCC ACG GAG AGC					
Pro Gln Val Phe Gly Lys Ser Asn Asp Gly Phe Val Pro Thr Glu Ser					
	30	35	40		
TAC GGA ACC ACT AGT GTG CAG AAT GTC TCA CAG ATC TTT GGG AGA AAT					
Tyr Gly Thr Thr Ser Val Gln Asn Val Ser Gln Ile Phe Gly Arg Asn					
	45	50	55		
GAC GAA AGT ACC ATG CCT ACA AGG AGC TAT GGA ACA GTC TGT CCC AGA					
Asp Glu Ser Thr Met Pro Thr Arg Ser Tyr Gly Thr Val Cys Pro Arg					
	60	65	70	75	
AAC TGG GAT TTT CAC CAA GGA AAA TGC TTT TTC TCC TTC TCC GAA					
Asn Trp Asp Phe His Gln Gly Lys Cys Phe Phe Ser Phe Ser Glu					
	80	85	90		

Fig. 11Z-1

TCA CCT TGG AAA GAC AGC ATG GAT TAT TGT GCA ACA CAA GGA TCC ACA	518
Ser Pro Trp Lys Asp Ser Met Asp Tyr Cys Ala Thr Gln Gly Ser Thr	95 100 105
CTG GCA ATT GTC AAC ACT CCA GAG AAA CTG AAG TAT CTT CAG GAC ATA	566
Leu Ala Ile Val Asn Thr Pro Glu Lys Leu Lys Tyr Leu Gln Asp Ile	110 115 120
GCT GGT ATT GAG AAT TAC TTT ATT GGT TTG GTA CGT CAG CCT GGA GAG	614
Ala Gly Ile Glu Asn Tyr Phe Ile Gly Leu Val Arg Gln Pro Gly Glu	125 130 135
AAA AAG TGG CGC TGG ATC AAC AAC TCT GTG TTC AAT GGC AAT GTT ACC	662
Lys Lys Trp Arg Trp Ile Asn Asn Ser Val Phe Asn Gly Asn Val Thr	140 145 150 155
AAT CAG GAC CAG AAC TTC GAC TGT GTC ACT ATA GGT CTG ACG AAG ACA	710
Asn Gln Asp Gln Asn Phe Asp Cys Val Thr Ile Gly Leu Thr Lys Thr	160 165 170
TAT GAT GCT GCA TCA TGT GAA GTC AGC TAT CGC TGG ATC TGC GAA ATG	758
Tyr Asp Ala Ala Ser Cys Glu Val Ser Tyr Arg Trp Ile Cys Glu Met	175 180 185

Fig. 11Z-2

AAT GCC AAA TGATCATAGA TCTCTACAAG AGTGAATTTT TACAGAGCTA	807
Asn Ala Lys	
190	
GCAAAGGAGA TTAGTTGTGA CTGAAACCAG CCCAGGAAAT ATAGAGCATC AAAGACTGTG	867
CCCATCTTCC ATAGGTGGAG TTCCCTATTG AATCCTCAAA GTCAATTTGT TACTCCACAA	927
ACATCTTCAC ATAGTAAAC TCCCTTTCTG ACCAAGTATT CCCTAAGACC ACACTTCCTG	987
TGAGAGGGGA CTGGATTCTA GTTATCTGCA GACAGAGCCA GGATTCTGGA GATGAAATCA	1047
ATATGGAAAT GCAGTCTGTT TCTGTAGAGC TGAGCCCTTTT AACTAATCAG TAGGGTTTGT	1107
TCTGTTGTCA GAACTGTTT ATCCTTAGAG AACATGCCCA CGCCACTGAG GAGAAACTGC	1167
TCGTGGAACA GATATGAGAA CTGTTAGGAA GCACTATGGG CAGAAGAATA TAAACTTGGC	1227
TTCACAAACAT CCCCCATTCC AGAAAGCCTC CCATTCCCAT ACAACATCGT AGAAGCAGAG	1287
GTCCCTTCTGA ATTGGGGAAG GACCTCTACA GCTCGACTTG GTACTGAACA AATATTGAGG	1347
GAATGAAGAA AGTTCTGAAT AGGACAGAGA TAAACAAGGA GGAGAAAGGAA AGAGATAGGA	1407
AGAAAGGAGA AGTGGGAAGG AGGGGAAAA GGAATGATGG GCAGGAGAAA AAGAGACAGG	1467
AGCAGCCAGG AAAAACACTC AAGCTAAAT TTTTTCAGGT TTTGGATAAA ATCTATTGTG	1527
ACATAAATAA TATCTTTTCA TTAGAAGAGA AAAGGCAAAA TTGGGGACAA ATGGGCACCA	1587
TGAGAGATGA AGCAGAGGTT AATTTGATCA CAAGGAAAAG AAGCAGGAA TGAGGTTGAA	1647
AACTTTTTGG ATACCTTGGC TGTTATCTCA AGAAGGTACA AGCTGCATAA AGTATAGGAG	1707
AAAAGAGATG TGCTGGTTGT TTTAAGTAGC AAAAATTAAA CTACAGAGAA GCCTATAGAA	1767
AGCTAAAGGA ATTAAAAACCA TCCAAATAATC AATTCATTAT TTTCAACTAA TAGCAATATG	1827
TATGTGCATT ACTAGTCAAA ATAAATTGTG AATTCTGTTA TTATAAAAAA AAAAAAAAG	1887
GGCGGCCGC	1896

Fig. 11Z-3

```

MI289 ATGAACTGGCACATGATCATCTCGGGGCTTATCGTAGTAGTGATCAAAGTTGTTGGAATG 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
HI289 ATGAACTGGCACATGATCATCTCTGGGCTTATTGTGGTAGTGCTTAAAGTTGTTGGAATG 60

MI289 ACCTTTTCTGCTGTATTTCCTCCACAGGTTTTTGGCAAAAGTAATGATGGCTTCGTCCCC 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
HI289 ACCTTATTCTACTTTATTTCCTCCACAGATTTTAAACAAAAGTAACGATGGTTTCACCCACC 120

MI289 ACGGAGAGCTACGGAACCACTAGTGTGCAGAAATGCTCTCACAGATCTTTGGGAGAAATGAC 180
      || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
HI289 ACCAGGAGCTATGGAACA-----GTCTCACAGATTTTGGGAGCAGTTCCTCCCAAGTCCC 174

MI289 GAAAGTACCATGCCCTACAAGGAGCTATGGAACAGTCTGTCCCAGAAACTGGGATTTTCAC 240
      | | ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
HI289 AACGGCTTCATTACCACAAGGAGCTATGGAACAGTCTGTCCCCCAAGACTGGGAAATTTTAT 234

MI289 CAAGGAAATGCTTTTCTCTCTCTCTCTCCGAATCACCTTGAAAGACAGCATGGATTAT 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
HI289 CAAGCAAGATGTTTTTCTTATCCACTTCTGAATCATCTTGGAATGAAAGCAGGGACTTT 294

```

Fig. 11Z-4


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MI289 ATGAACTGGCACATGATCATCTCGGGGCTTATCGTAGTAGTCAAAAGTTGTTGGAATG 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
HI289 ATGAACTGGCACATGATCATCTCGGGGCTTATCGTAGTAGTCAAAAGTTGTTGGAATG 60

MI289 ACCTTTTTCTGCTGTATTTCCCCACAGGTTTTTTGGCAAAAGTAATGATGGCTTCGTCCCC 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
HI289 ACCTTATTTCTACTTTATTTCCCCACAGATTTTAAACAAAAGTAACGATGGTTTCACCCACC 120

MI289 ACGGAGAGCTACGGAACCACTAGTGTGCAGAAATGTCTCACAGATCTTTGGGAGAAATGAC 180
      || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
HI289 ACCAGGAGCTATGGAACA-----GTCTCACAGATTTTGGGAGCAGTTCCCCCAAGTCCC 174

MI289 GAAAGTACCATGCCCTACAAGGAGCTATGGAACAGTCTGTCCCAGAAACTGGGATTTTCAC 240
      | | ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
HI289 AACGGCTTCATTACCACAAGGAGCTATGGAACAGTCTGCCCCCAAGACTGGGAATTTTAT 234

MI289 CAAGGAAAATGCTTTTCTCTCCTTCTCCGAATCACCTTGAAAGACAGCATGGATTAT 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
HI289 CAAGCAAGATGTTTTTCTTATCCACTTCTGAATCATCTTGGAATGAAAGCAGGGACTTT 294

```

Fig. 11Z-4

```

MI289  TGCGAACAAGGATCCACACTGGCAATTGTCAACACTCCAGAGAAAACCTGAAGTATCTT 360
      || | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
HI289  TGCAAAAGGAAAAGGATCCACATTGGCAATTGTCAACACGCCAGAGAAAACCTGAAGTTTCTT 354

MI289  CAGGACATAGCTGGTATTGAGAAATTACTTTATTGGTTTGGTACGTCAGCCTGGAGAGAAA 420
      ||||| ||| | ||||| || ||||| || | || | || |||||
HI289  CAGGACATAACTGATGCTGAGAAAGTATTTTATTGGCTTAATTACCATCGTGAAGAGAAA 414

MI289  AAGTGGCGCTGGATCAACAACCTCTGTGTTCAATGGCAATGTTACCAATCAGGACCAGAAC 480
      | ||||| ||||| ||||| ||||| ||||| ||||| |||||
HI289  AGTGGCGTTGGATCAACAACCTCTGTGTTCAATGGCAATGTTACATCATCCAATCAGAAT 474

MI289  TTCGACTGTGTCACTATAGGTCTGACGAAGACATATGATGCTGCATCATGTGAAGTCAGC 540
      | | | | | | | | | | | | | | | | | | | | | |
HI289  CAGAAATTCAACTGTGCGACCATTTGGCCCTAACAAAGACATTTGATGCTGGTGACATCAGC 534

MI289  TATCGCTGGATCTGCGAAATGAATGCCAAA 570
      || ||| ||||| || | ||||| |||||
HI289  TACCGCAGGATCTGTGAGAAAGAAATGCCAAA 564

```

Fig. 11Z-5

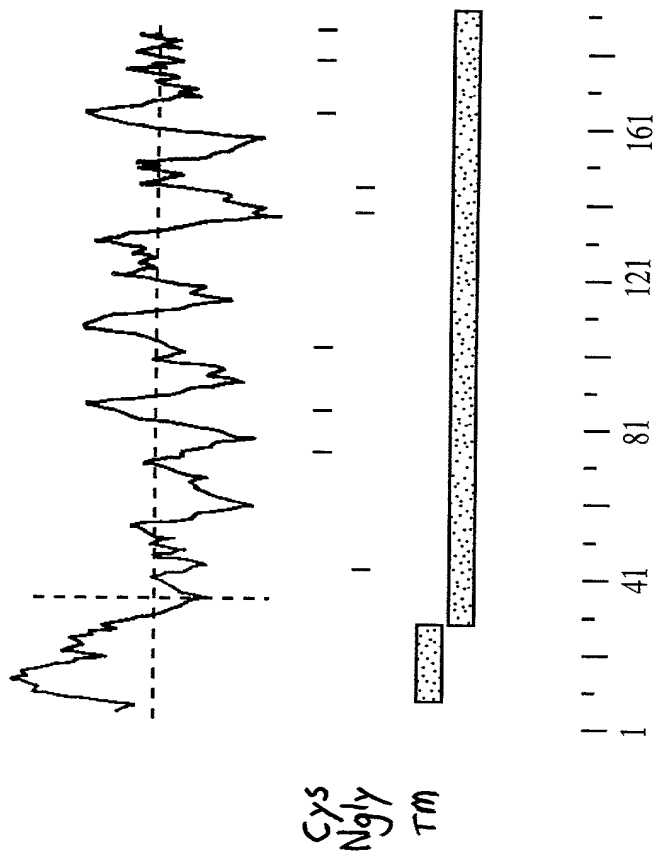


FIG. 11Z-6

L	F	L	G	G	V	G	M	V	G	T	V	A	V	T	V	M	P	Q	19	
G	CTG	TTT	CTT	GGT	GGT	GTT	GGA	ATG	GTG	GGC	ACA	GTG	GCT	ACT	GTC	ATG	CCT	CAG	58	
W	R	V	S	A	F	I	E	N	N	I	V	V	F	E	N	F	W	E	G	39
TGG	AGA	GTG	TCG	GCC	TTC	ATT	GAA	AAC	AAC	ATC	ATC	GTG	GTT	TTT	GAA	AAC	TTC	TGG	GAA	118
L	W	M	N	C	V	R	Q	A	N	I	R	M	Q	C	K	I	Y	D	S	59
CTG	TGG	ATG	AAT	TGC	GTG	AGG	CAG	GCT	AAC	ATC	AGG	ATG	CAG	TGC	AAA	ATC	TAT	GAT	TCC	178
L	L	A	L	S	P	D	L	Q	A	A	R	G	L	M	C	A	A	S	V	79
CTG	CTG	GCT	CTT	TCT	CCG	GAC	CTA	CAG	GCA	GCC	AGA	GGA	CTG	ATG	TGT	GCT	GCT	TCC	GTG	238
M	S	F	L	A	F	M	M	A	I	L	G	M	K	C	T	R	C	T	G	99
ATG	TCC	TTC	TTG	GCT	TTC	ATG	ATG	GCC	ATC	CTT	GGC	ATG	AAA	TGC	ACC	AGG	TGC	ACG	GGG	298
D	N	E	K	V	K	A	H	I	L	L	T	A	G	I	I	F	I	I	T	119
GAC	AAT	GAG	AAG	GTG	AAG	GCT	CAC	ATT	CTG	CTG	ACG	GCT	GGA	ATC	ATC	TTC	ATC	ATC	ACG	358
G	M	V	V	L	I	P	V	S	W	V	A	N	A	I	I	R	D	F	Y	139
GGC	ATG	GTG	GTG	CTC	ATC	CCT	GTG	AGC	TGG	GTT	GCC	AAT	GCC	ATC	ATC	AGA	GAT	TTC	TAT	418
N	S	I	V	N	V	A	Q	K	R	E	L	G	E	A	L	Y	L	G	W	159
AAC	TCA	ATA	GTG	AAT	GTT	GCC	CAA	AAA	CGT	GAG	CTT	GGA	GAA	GCT	CTC	TAC	TTA	GGA	TGG	478

Fig. 12A

T	T	A	L	V	L	I	V	G	G	A	L	F	C	C	V	F	C	C	N	179
ACC	ACG	GCA	CTG	GTG	CTG	ATT	GTT	GGA	GGA	GCT	CTG	TTC	TGC	TGC	GTT	TTT	TGT	TGC	AAC	538
E	K	S	S	S	Y	R	Y	S	I	P	S	H	R	T	T	Q	K	S	Y	199
GAA	AAG	AGC	AGT	AGC	TAC	AGA	TAC	TCG	ATA	CCT	TCC	CAT	CGC	ACA	ACC	CAA	AAA	AGT	TAT	598
H	T	G	K	K	S	P	S	V	Y	S	R	S	Q	Y	V	*				215
CAC	ACC	GGA	AAG	AAG	TCA	CCG	AGC	GTC	TAC	TCC	AGA	AGT	CAG	TAT	GTG	TAG				649
TTGTG	TATG	TTTTTTT	TAACTTT	TACTATA	AAAGCC	ATGCA	AAAAAT	CTATAT	TACTTT	CTCA	AAAAAT	GGACCC	CAA							728
AGAA	ACTTT	TGATTT	TACTGT	TCTTAA	CTGCTT	AACTT	AACTAC	AGAACT	GTGCAT	CAGCTAT	TATGAT	TCTATA	AGC							807
TATTT	CAGC	AGAA	TGAGAT	ATTAA	CCCAAT	GCTTT	GATTG	TTCTAG	AAAGTAT	AGTAAT	TTGTTT	CTAAG	GGTTC							886
AAGCA	TCTACT	CTTTT	TATCAT	TTTACT	TCAAA	ATGACAT	TGCTAA	AGACTG	CAATAT	TTTACT	ACTGTA	ATTTCT	CCAC							965
GACAT	AGCAT	TATGT	ACATAG	ATGAG	TGTAAC	ATTATAT	CTCAC	ATAGAC	ATGCTT	ATATG	TGTTT	TATTT	AAAATG							1044
AAATG	CCAGT	CCATT	ACACT	GAATA	AAATAG	AACTCA	ACTATT	GCTTTT	CAGG	AAATCAT	GGATAG	GGTTGA	AGAAAGT							1123
TACTAT	TAAAT	TGTTT	AAAAAC	AGCTT	AGGAT	TAAATG	TCTCC	ATTATA	ATGA	AGATTAA	AAATGA	AGGCTT	TAATCAG							1202
CATTG	TAAAGG	AAATGA	ATGG	CTTCT	GATATG	CTGTTT	TTTAG	CCTAGG	AGTTAG	AAATCCT	AACTTCT	TTTATC	CTC							1281
TTCTCC	AGAGG	CTTTTT	TTTTT	CTTG	TATTA	AAATTA	ACATTT	TAAAA	AGCAG	ATATTT	TGTCA	AGGG	CTTTGCAT							1360
TCAA	ACTG	CTTTCC	AGGCTAT	ACTC	AGAA	AGATA	AAAGT	GTGAT	CTA	AGAAAA	AGTGA	TGTTT	TAGGAA	AGT						1439
AAAA	TATTT	TGTTTT	TGTA	TTTGA	AGAA	ATGATG	CAATTT	TGAC	AGAAAT	CATATAT	GTATG	GATAT	TTTAA	ATA						1518
AGTAT	TGAG	TACAG	ACTTT	GAGG	TTTCAT	CAATATA	ATAA	TAAG	AGCAG	AAAAATAT	GTCTT	GTTTT	CATTTG	CTTA						1597

Fig. 12B

CCAAAAAACAACAAAAAGTTGTCCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTGTCA 1676
 TTTTGTCTCTGTGAAAAATAAAATTTCCCTTCTGTACCAATTTCTGTTAGTTTACTAAAACTGTAAATACGTATTTT 1755
 TCTGTTTATCCAAATTTGATGAAACTGACAAATCCAATTTGAAAGTTTGTGTCGACGTCGTCTAGCTTAAATGAATGT 1834
 GTTCTATTTGCTTTATACATTTATATTAATAAATTGTACATTTTCTAAAAAATAAAAAAATAAAAAA 1909

Fig. 12C

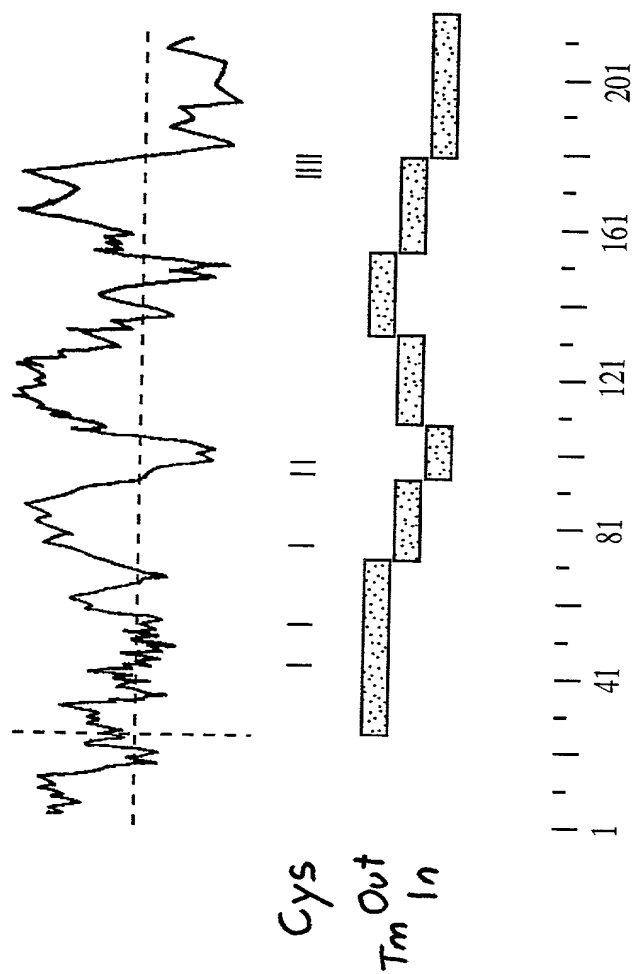


FIG. 12D

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DKFZ G-----GGGCA-----
:
I309 GCTGTTCTTGGTGGTGGTGGGACAGTGGCTGTCACTGTGCCTCAGTGGAGAGTGTCG
      10      20      30      40      50      60      70

DKFZ -----

I309 GCCTTCATTGAAAAACAACATCGTGGTTTTTGAAAACTTCTGGGAAGGACTGTGGATGAATTGCCGTGAGGC
      80      90      100     110     120     130     140

DKFZ -----

I309 AGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTTTCTCCGGACCTACAGGCAGC
      150     160     170     180     190     200     210

DKFZ -----

I309 CAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCCTTCTTGGCTTTCAATGATGGCCATCCTTGGCATGAAA
      220     230     240     250     260     270     280

DKFZ -----

I309 TGCACCAAGTGCACGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCA
      290     300     310     320     330     340     350

```

Fig. 12E

DKFZ -----

I309 TCATCACGGGCATGGTGGTCTCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCATATAA
360 370 380 390 400 410 420

DKFZ -----

I309 CTCAATAGTGAATGTTGCCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTG
430 440 450 460 470 480 490

DKFZ -----

I309 GTGCTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTTGTGCAACGAAAAAGCAGTAGCTACAGAT
500 510 520 530 540 550 560

DKFZ -----

I309 ACTCGATACCTTCCCATCGCACAAACCCAAAAAAGTTATCACACCGGAAAGAGTCACCGAGCGTCTACTC
570 580 590 600 610 620 630

DKFZ -----

I309 CAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTTAACTTTACTATAAAGCCATGCAAATGACAAAAATC
640 650 660 670 680 690 700

Fig. 12F

```

DKFZ -----
I309 TATATTACTTTCTCAAAATGGACCCCAAGAAACTTTGATTACTGTTCTTAACTGCCCTAATCTTAATTA
      710      720      730      740      750      760      770
DKFZ -----
      10      20
      -----GAA TGAGATATTAAACCCAATGC
      .....
I309 CAGGAACTGTGCATCAGCTATTATGATTCTATAAGCTATTTTCAGCAGAAATGAGATATTAAACCCAATGC
      780      790      800      810      820      830      840
      30      40      50      60      70      80      90
DKFZ TTTGATTGTTCTAGAAAAGTATAGTAATTTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTATCATTT
      .....
I309 TTTGATTGTTCTAGAAAAGTATAGTAATTTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTATCATTT
      850      860      870      880      890      900      910
      100      110      120      130      140      150      160
DKFZ ACTTCAAAATGACATTGCTAAAGACTGCATTATTTTACTACTGTAAATTTCTCCACGACATAGCATTTATGT
      .....
I309 ACTTCAAAATGACATTGCTAAAGACTGCATTATTTTACTACTGTAAATTTCTCCACGACATAGCATTTATGT
      920      930      940      950      960      970      980

```

Fig. 12G

```

170      180      190      200      210      220      230
DKFZ ACATAGATGAGTGTAACATTTATATCTCACATAGAGACATGCTTATATGGTTTATTTAAATGAAATGC
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 ACATAGATGAGTGTAACATTTATATCTCACATAGAGACATGCTTATATGGTTTATTTAAATGAAATGC
      990      1000      1010      1020      1030      1040      1050

240      250      260      270      280      290      300
DKFZ CAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGAAATCATGGATAGGGTTGAAGAA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 CAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGAAATCATGGATAGGGTTGAAGAA
      1060      1070      1080      1090      1100      1110      1120

310      320      330      340      350      360      370
DKFZ GGTACTATTAAATGTTTAAACAGCTTAGGGATTAAATGTCCTCCATTTATAATGAAGATTAAATGA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 GGTACTATTAAATGTTT-AAACAGCTTAGGGATTAAATGTCCTCCATTTATAATGAAGATTAAATGA
      1130      1140      1150      1160      1170      1180

380      390      400      410      420      430      440
DKFZ AGGCTTTAATCAGCATTTGTAAAGGAAATTTGAATGGCTTTCTGATATGCTGTTTTTAGCCTAGGAGTTAG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 AGGCTTTAATCAGCATTTGTAAAGGAAATTTGAATGGCTTTCTGATATGCTGTTTTTAGCCTAGGAGTTAG
      1190      1200      1210      1220      1230      1240      1250

```

Fig. 12H

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450      460      470      480      490      500      510
DKFZ AAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTCTTGTATTAATTAACATTTTTAA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 AAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTCTTGTATTAATTAACATTTTTAA
1260 1270 1280 1290 1300 1310 1320

520      530      540      550      560      570      580
DKFZ AAAGCAGATATTTGTCAAGGGGCTTTGCATTCAAACCTGCTTTCCAGGGCTATACTCAGAAAGAGATA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 AAAGCAGATATTTGTCAAGGGGCTTTGCATTCAAACCTGCTTTCCAGGGCTATACTCAGAAAGAGATA
1330 1340 1350 1360 1370 1380 1390

590      600      610      620      630      640      650
DKFZ AAAGTGTGATCTAAGAAAAGTGATGGTTTtaggaaaAGTGAATAATTTTGTGTTTGTATTGAAGAAG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 AAAGTGTGATCTAAGAAAAGTGATGGTTTtaggaaaAGTGAATAATTTTGTGTTTGTATTGAAGAAG
1400 1410 1420 1430 1440 1450 1460

660      670      680      690      700      710      720
DKFZ AATGATGCATTTTGACAAGAAAATCATATATGTATGGATATATTTAATAAGTATTTGAGTACAGACTTTG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 AATGATGCATTTTGACAAGAAAATCATATATGTATGGATATATTTAATAAGTATTTGAGTACAGACTTTG
1470 1480 1490 1500 1510 1520 1530

```

Fig. 12I

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730      740      750      760      770      780      790
DKFZ AGGTTTCATCAATATAAAAGAGCAGAAAATATGCTCTGGTTTTCATTTGCTTACCAAAAAACAA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 AGGTTTCATCAATATAAAAGAGCAGAAAATATGCTCTGGTTTTCATTTGCTTACCAAAAAACAA
1540      1550      1560      1570      1580      1590      1600

800      810      820      830      840      850      860
DKFZ CAACAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTATGTGGTACCTGAGTCAAAATTGTCATTT
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 CAACAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTATGTGGTACCTGAGTCAAAATTGTCATTT
1610      1620      1630      1640      1650      1660      1670

870      880      890      900      910      920      930
DKFZ TTGTTCTGTGAAAAATAAATTCCCTTCTGTACCATTTCTGTTAGTTTACTAAATCTGTAAATACTG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 TTGTTCTGTGAAAAATAAATTCCCTTCTGTACCATTTCTGTTAGTTTACTAAATCTGTAAATACTG
1680      1690      1700      1710      1720      1730      1740

940      950      960      970      980      990      1000
DKFZ TATTTTCTGTTTATTCCAAATTGATGAAACTGACAATCCAATTTGAAAGTTTGTGTCGACGCTGTCT
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 TATTTTCTGTTTATTCCAAATTGATGAAACTGACAATCCAATTTGAAAGTTTGTGTCGACGCTGTCT
1750      1760      1770      1780      1790      1800      1810

```

Fig. 12J

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1010      1020      1030      1040      1050      1060      1070
DKFZ AGCTTAAATGAATGTTCTATTGCTTTATACATTATATAATAAATTGTACATTTTCCAAAAAAA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 AGCTTAAATGAATGTTCTATTGCTTTATACATTATATAATAAATTGTACATTTTCTAAAAAAA
1820      1830      1840      1850      1860      1870      1880

1080      1090
DKFZ AAAAAAAAAA-----
      ::::::::::::::
I309 AAAAAAAAAAAAAAAAAAAAAA
1890      1900

```

Fig. 12K

[illegible]

Fig. 12L

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260      270      280      290      300      310      320
I309 CTTTCATGATGGCCATCCTTGGCATGAAATGCACCAAGTGCACGGGGCAATGAGAAGTGAAAGGCTCA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CLAUD8 CTTTCATGACAGCCATCCTCGGAATGAAGTGCACCAAGTGCACGGGGACGATGAGAACGTGAAGAGCCG
      290      300      310      320      330      340      350

330      340      350      360      370      380      390
I309 CATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCAATGGTGGTCTCATCCCTGTGAGCTGGGTT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CLAUD8 CATCTTGCTGACAGCCGGAATCATCTTCTTCATCACCGGCTTGGTTGTGCTCATCCCTGTGAGCTGGGTT
      360      370      380      390      400      410      420

400      410      420      430      440      450      460
I309 GCCAATGCCATCATCAGAGATTTCATAAATCAATAGTGAATGTGCCCAAAAACGTGAGCTTGGAGAAG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CLAUD8 GCCAATTCCATCATCAGAGACTTCTACAACCCACTGGTGGATGTGGCCCTAAAGCGCGAGCTGGGAGAAG
      430      440      450      460      470      480      490

470      480      490      500      510      520      530
I309 CTCTCTACTTAGGATGGACCACGGCACTGGTGTGCTGATTGTTGGAGGAGCTCTGTCTGCTGCGTTTGTG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CLAUD8 CCCTCTACATAGGCTGGACCACAGCGCTGGTGTGCTGATCGCTGGAGGAGCACTGTTCTGTGTGTTTGTG
      500      510      520      530      540      550      560

```

Fig. 12M


```

540      550      560      570      580      590      600
I309 TTGCAACGAAAAGAGCAGTAGCTACAGATACTCGATACTTCCCATCGCACAAACCCAAAAGTTATCAC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CLAUD8 TTGTACTGAAAGGAGCAACAGTTACAGGTACTCGGTACCATCCCATCGCACCACTCAACGGAGTTTCCAC
      570      580      590      600      610      620      630

610      620      630      640      650      660      670
I309 ACCGGAAGAAGTCACCGAGCGTCTACTCCAGAAAGTCAGTATGTGTAGTTGTGTATGTTTTTTAACTTT
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
CLAUD8 GCCGAAAAGAGATCTCCGAGCATATACTCCAAAAGTCAGTATGTGTAG-----
      640      650      660      670

680      690      700      710      720      730      740
I309 ACTATAAGCCATGCAAAATGACAAAATCTATATTACTTTCTCAAAATGGACCCCAAGAAACTTTTGATT
CLAUD8 -----

750      760      770      780      790      800      810
I309 TACTGTTCTTAAGTGCCTAATCTTAATTACAGGAAGTGTGCATCAGCTATTATGATTTCTATAAGCTATT
CLAUD8 -----

```

Fig. 12N

	820	830	840	850	860	870	880
I 309	TCAGCAGAATGAGATAATTAAACCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTGTTTTCTAAGGT						
CLAUD8	-----						
	890	900	910	920	930	940	950
I 309	GGTTCAAGCATCTACTCTTTTATCATTTACTTCAAAATGACATTGCTAAAGACTGCATTATTTTACTAC						
CLAUD8	-----						
	960	970	980	990	1000	1010	1020
I 309	TGTAATTTCTCCACGACATAGCATTTATGTACATAGATGAGTGTAACATTTATATCTCACATAGAGACATG						
CLAUD8	-----						
	1030	1040	1050	1060	1070	1080	1090
I 309	CTTATATGGTTTTATTAAATGAAATGCCAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTT						
CLAUD8	-----						
	1100	1110	1120	1130	1140	1150	1160
I 309	TCAGGAAATCATGGATAGGGTTGAAGAAGGTTACTATTAAATGTTAAAAACAGCTTAGGGATTAAATGT						
CLAUD8	-----						

Fig. 120

	1170	1180	1190	1200	1210	1220	1230
I 309	CCTCCATT	TATAATGA	GATTAAAT	GAGGCTT	AATCAGCA	TTGTAAGG	AAATTGAA
							TGGCTTTCTG
CLAUD8	-----						
	1240	1250	1260	1270	1280	1290	1300
I 309	ATATGCTG	TTTTAGCC	TAGGAGTT	AGAAATCC	TAACTTCT	TATCCTCT	CTCCCAGAG
							GCTTTTTTTT
CLAUD8	-----						
	1310	1320	1330	1340	1350	1360	1370
I 309	TTCTTGTG	TATAAATA	ACAATTTT	TAAAAAGC	AGATATTT	TGTCAAGG	GGCTTGCATT
							CAAACTGCTT
CLAUD8	-----						
	1380	1390	1400	1410	1420	1430	1440
I 309	TTCCAGGG	CTATACT	CAGAAAG	AATAAAAG	TGTGATCT	AAGAAAAA	AGTGATGTTT
							TAGGAAAGTGAA
CLAUD8	-----						

Fig. 12P

```

1450      1460      1470      1480      1490      1500      1510
I309 AATATTTTGTGTTTGTATTTGAAGAAGATGATGCATTTTGACAAGAAATCATATATGTATGGATATAT
CLAUD8 -----

1520      1530      1540      1550      1560      1570      1580
I309 TTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAATAAAAGAGCAGAAAAATATGTCTT
CLAUD8 -----

1590      1600      1610      1620      1630      1640      1650
I309 GGTTTTCATTTGCTTACCAAAAAACAACAACAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTAT
CLAUD8 -----

1660      1670      1680      1690      1700      1710      1720
I309 GTGGGTACCTGAGTCAAAATTGTCATTTTGTCTGTGAAAAATAAATTTCTTCTTGTAACCATTTCTGT
CLAUD8 -----

1730      1740      1750      1760      1770      1780      1790
I309 TTAGTTTACTAAAAATCTGTAAATACTGTATTTTCTGTATTATCCAAATTTGATGAAACTGACAATCCA
CLAUD8 -----

```

Fig. 12Q

	1800	1810	1820	1830	1840	1850	1860
I309	ATTGAAAGTTTGTGTCGACGCTCTGTCTAGCTTAAATGAATGTGTTCTATTGCTTTATACATTATATT						
CLAUD8	-----						
I309	AATAAATTGTACATTTTCTAAAAAATAAAAAAAAAAAAAA						
CLAUD8	-----						

Fig. 12R

```

CLAUD8 MATYALQMAALVLGGVMGTVAVTIMQPWRVSAFIESNIVVFENRWEGLMNCMRHANIRMCKVYDSL
I309 -----LFLGGVMGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLMNCVRQANIRMQCKIYDSL
      10    20    30    40    50    60    70

CLAUD8 LALSPDLQASRGLMCAASVLAFLAFMTAILGMKCTRCTGDDENVKSRILLTAGIIFFITGLVVLIIPVSWV
I309 LALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGIIFIITGMVVLIIPVSWV
      70    80    90   100   110   120   130

CLAUD8 ANSIIRDfYNPLVDVALKRELGEALYIGWTTALVLIAGGALFCCVFCCTERSNSYRVSPSHRTTQRSFH
I309 ANAIIRDfYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCKEKSSSYRYSIPIPSHRTTQKSYH
      140   150   160   170   180   190   200

CLAUD8 AEKRSPSIYSKSQYV
I309 TGKKSPSVYSRSQYV
      210

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Fig. 12S

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I309 .....LFLGGVMVGTVAVTMPQWRVSAFIENNIIVFFENFWEGL 40
hCPE MASMGLQVMGIALAVLGLAVMLCCALPMWRVTAFIGSNIIVTSQTIWEGL 50
mCPE MASMGLQVLGISLAVLGLGIIILSCALPMWRVTAFIGSNIIVTAQTSWEGL 50
rRPV .MSMSLEITGTSLAVLGLWLTIVCCALPMWRVSAFIGSSIITAQITWEGL 49

I309 WMNCVRQANIRMQCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAIL 90
hCPE WMNCVVQSTGQMCKVYDSSLALPQDLQAARALVISIIVAALGVLLSVV 100
mCPE WMNCVVQSTGQMCKMYDSSLALPQDLQAARALMVISIIVGALGMLLSVV 100
rRPV WMNCV.QSTGQMCKMYDSSLALPQDLQAARALIVSILLAAGLLVALV 98

I309 GMKCTRCTGDNEKVKAHILLTAGIIFIITGMVVLIIPVSWVANAIIRDFYN 140
hCPE GGKCTNCLED.ESAKAKTMIVAGVVFLLAGLMVIVPVSWTAHNI IQDFYN 149
mCPE GGKCTNCMED.ETVKAKIMITAGAVFIVASMLIMVPVSWTAHNVIRDFYN 149
rRPV GAQCTNCVQD.ETAKAKITIVAGVLFLLAAVITLVPVSWSANTIIRDFYN 147

I309 SIVNVAQKRELGEALYLGWTTALVLI VGGALFCCVFCCKNEKSSSYRYSIP 190
hCPE PLVASGQKREMGASLYVGWAAAGLLLLGGGLICC.NCPRTDKPYSAKYS 198
mCPE PMVASGQKREMGASLYVGWAAAGLLLLGGGLCCSCPPRSNDKPYSAKYS 199
rRPV PLVPEAQKREMGTGLYVGWAAAALQLLGGALLCCSCPPREKYAPTILYS 197

I309 SHRTTQKSYHTGKKSPSVYSRSQYV 215
hCPE AARSAAAASNYV..... 209
mCPE AARSVPASNYV..... 210
rRPV APRSTGPGTGTAYDRKTTSERPGARTPHHHHYQPSMYPTRPACSLASET 248

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Fig. 12T

CGAGCGCGCGCGGCAGGTCAGACATGGGCCAAGAGCCAGAGCCCGTCCGGGGTCTGTGAGTTGAGCTTGAGGCCG 79

M R V I M G I A S L G F L W A V F L 18

CAGG ATG AGG GTC ATC ATG GGG ATA GCC AGC CTG GGG TTC CTC TGG GCA GTA TTC CTG 137

L P L V F G V P T E E T T F G E S V A S 38

CTT CCT CTT GTG TTT GGG GTC CCC ACA GAG GAG ACT ACC TTT GGA GAA TCT GTG GCC TCC 197

H L P K G C R R C C D P E D L M S S D D 58

CAT CTC CCC AAA GGC TGT CGA CGA TGC TGT GAC CCC GAG GAC CTG ATG TCC TCT GAT GAT 257

T V Q A P V S P Y V L P E V R P Y L G R 78

ACG GTC CAG GCC CCT GTT TCC CCT TAT GTC CTG CCT GAA GTC AGG CCG TAC CTC GGC CGC 317

D H 80

GAC CAC 323

124/361

Fig. 13A

CGGACGCGTGGCGGACGCGTGGGGTTATTCTTTGGTTGTTAGGTATAATATGGGCATTTAAAAACAACACCCAGTTT 79

 M E F L Y R I V V G F I L I F T 16

TGTA CTTGTATAAGT ATG GAA TTC TTA TAT TAT AGG ATT GTT GTT GGA TTC ATT CTT ATC TTT ACA 142

F F N I K G Q N T K C P M S C Y Y I V R 36

TTT TTT AAT ATT AAG GGA CAG AAT ACC AAG TGT CCA ATG TCT TGT TAT TAT ATT GTT AGG 202

V L G T L G I L T V F W V C P L T I F N 56

GTA CTG GGC ACT TTG GGG ATA TTG ACT GTA TTC TGG GTT TGC CCC CTC ACT ATT TTT AAT 262

P D Y F I P I S I T I V L T L L L G I L 76

CCA GAC TAT TTT ATA CCT ATC AGT ATA ACT ATA GTT CTT ACT CTT CTT CTT GGA ATT CTT 322

F L I V Y Y G S F H P N R S A E T K C D 96

TTT CTT ATT GTT TAT TAT GGG AGT TTT CAC CCA AAC AGA AGT GCA GAA ACA AAA TGT GAT 382

E I D G K P V L R E C R M R Y F L M E * 115

GAA ATT GAT GGA AAA CCA GTT CTA AGA GAA TGT AGA ATG AGA TAT TTC CTA ATG GAA TAA 442

GCTATTCA TTTATGATATATATTTCTTATATTTTGTTCATTTGTTAGTAAAGAAAATGTGTGTTAAAAA 521

AAAAAAAAAAAAAAAAAAAAA 546

Fig. 14A

CGGACGCGGTGGCGGACGCGTGGGCAGCTGAAGAAAGAGAGGA	M	K	R	L	L	L	L	L	F	8
										68
L F F I T F S S A F P L V R M T E N E E										28
TTG TTC TTT ATA ACA TTT TCT TCT GCA TTT CCC TTA GTC CGG ATG ACG GAA AAT GAA GAA										128
N M Q L A Q A Y L N Q F Y S L E I E G N										48
AAT ATG CAA CTG GCT CAG GCA TAT CTC AAC CAG TTC TAC TCT CTT GAA ATA GAA GGG AAT										188
H L V Q S K N R S L I D D K I R E M Q A										68
CAT CTT GTT CAA AGC AAG AAT AGG AGT CTC ATA GAT GAC AAA ATT CGG GAA ATG CAA GCA										248
F F G L T V T G K L D S N T L E I M K T										88
TTT TTT GGA TTG ACA GTG ACT GGA AAA CTG GAC TCA AAC ACC CTT GAG ATC ATG AAG ACA										308
P R C G V P D V G Q Y G Y T L P G W R K										108
CCC AGG TGT GGG GTG CCT GAT GTG GGC CAG TAT GGC TAC ACC CTC CCT GGG TGG AGA AAA										368
Y N L T Y R I I N Y T P D M A R A A V D										128
TAC AAC CTC ACC TAC AGA ATA ATA AAC TAT ACT CCG GAT ATG GCA CGA GCT GCT GTG GAT										428
E A I Q E G L E V W S K V T P L K F T K										148
GAG GCT ATC CAA GAA GGT TTA GAA GTG TGG AGC AAA GTC ACT CCA CTA AAA TTC ACC AAG										488

Fig. 15A

I S K G I A D I M I A F R T R V H G R C 168
 ATT TCA AAG GGG ATT GCA GAC ATC ATG ATG ATT GCC TTT AGG ACT CGA GTC CAT GGT CGG TGT 548

 P R Y F D G G P L G V L G H A F P P G P G 188
 CCT CGC TAT TTT GAT GGT CCC TTG GGA GTG CTT GGC CAT GCC TTT CCT CCT GGT CCG GGT 608

 L G G D T H F D E D E N W T K D G A G F 208
 CTG GGT GGT GAC ACT CAT TTT GAT GAG GAT GAA AAC TGG ACC AAG AAG GAT GGA GCA GGA TTC 668

 N L F L V A A H E F G H A L G L S H S N 228
 AAC TTG TTT CTT GTG GCT GCT CAT GAA TTT GGT CAT GCA CTG GGG CTC TCT CAC TCC AAT 728

 D Q T A L M F P N Y V S L D P R K Y P L 248
 GAT CAA ACA GCC TTG ATG TTC CCA AAT TAT GTC TCC CTG GAT CCC AGA AAA TAC CCA CTT 788

 S Q D D I N G I Q S I Y G G L P K V P A 268
 TCT CAG GAT GAT ATC AAT GGA ATC CAG TCC ATC TAT GGA GGT CTG CCT AAG GTA CCT GCT 848

 K P K E P T I P H A C D P D L T F D A I 288
 AAG CCA AAG GAA CCC ACT ATA CCC CAT GCC TGT GAC CCT GAC TTG ACT TTT GAC GCT ATC 908

 T T F R R E V M F F K G R H L W R I Y Y 308
 ACA ACT TTC CGC AGA GAA GTA ATG TTC TTT AAA GGC AGG CAC CTA TGG AGG ATC TAT TAT 968

Fig. 15B

D I T D V E F E L I A S F W P S L P A D 328
 GAT ATC ACG GAT GTT GAG TTT GAA TTA ATT GCT TCA TTC TGC CCA TCT CTG CCA GCT GAT 1028

 L Q A A Y E N P R D K I L V F K D E N F 348
 CTG CAA GCT GCA TAC GAG AAC CCC AGA GAT AAG ATT CTG GTT TTT AAA GAT GAA AAC TTC 1088

 W M I R G Y A V L P D Y P K S I H T L G 368
 TGG ATG ATC AGA GGA TAT GCT GTC TTG CCA GAT TAT CCC AAA TCC ATC CAT ACA TTA GGT 1148

 F P G R V K K I D A A V C D K T T R K T 388
 TTT CCA GGA CGT GTG AAG AAA ATA GAT GCA GCC GTC TGT GAT AAG ACC ACA AGA AAA ACC 1208

 Y F F V G I W C W R F D E M T Q T M D K 408
 TAC TTC TTT GTG GGC ATT TGG TGC TGG AGG TTT GAT GAA ATG ACC CAA ACC ATG GAC AAA 1268

 G F P Q R V V K H F P G I S I R V D A A 428
 GGA TTC CCG CAG AGA GTG GTA AAA CAC TTT CCT GGA ATC AGT ATC CGT GTT GAT GCT GCT 1328

 F Q Y K G F F F F F S R G S K Q F E Y N I 448
 TTC CAG TAC AAA GGA TTC TTC TTT TTC AGC CGT GGA TCA AAG CAA TTT GAA TAC AAC ATT 1388

 K T K N I T R I M R T N T W F Q C K E P 468
 AAG ACA AAG AAT ATT ACC CGA ATC ATG AGA ACT AAT ACT TGG TTT CAA TGC AAA GAA CCA 1448

Fig. 15C

K	N	S	S	F	G	F	D	I	N	K	E	K	A	H	S	G	G	I	K	488																														
AAG	AAC	TCC	TCA	TTT	GGT	TTT	GAT	ATC	AAC	AAG	GAA	AAA	GCA	CAT	TCA	GGA	GGC	ATA	AAG	1508																														
I	L	Y	H	K	S	L	S	L	F	I	F	G	I	V	H	L	L	K	N	508																														
ATA	TTG	TAT	CAT	AAG	AGT	TTA	AGC	TTG	TTT	ATT	TTT	GGT	ATT	GTT	CAT	TTG	CTG	AAA	AAC	1568																														
T	S	I	Y	Q	*															514																														
ACT	TCT	ATT	TAT	CAA	TAA															1586																														
ATT																				CAT	AGACCT	AAAA	TAA	AA	CCT	CA	AC	AGG	CT	TTT	TAA	TATA	AA	AT	CT	GC	TT	CA	AA	AT	AG	AA	TAA	AA	CC	AT	TCT	TT	AAC	1665
AAC																				AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	1684												

Fig. 15D

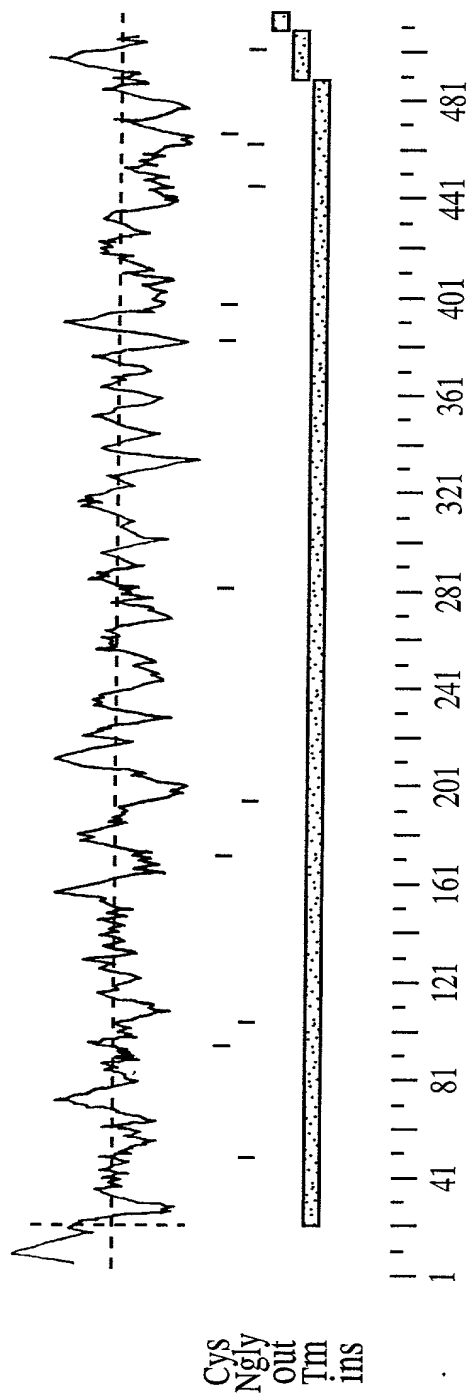


FIG. 15E

GCTTTAACTGAAGACAGCAATG															M	K	C	L	L	S	L	M	V	N	F	I	T	13
GCTTTAACTGAAGACAGCAATG															AAG	ATG	TGC	CTT	CTG	TCT	CTG	ATG	GTT	AAT	TTT	ATA	ACA	60
L	S	A	A	F	P	P	D	R	K	D	K	N	E	E	N	N	Q	L	A									33
CTT	TCC	GCT	GCA	TTT	CCT	CCA	GAC	AGG	AAG	GAC	AAA	AAT	GAG	GAG	AAC	AAC	CAA	CTG	GCC									120
Q	A	Y	L	N	Q	F	Y	S	L	E	I	E	G	S	H	F	V	Q	S									53
CAG	GCA	TAT	CTC	AAC	CAG	TTC	TAC	TCT	CTT	GAA	ATA	GAA	GGG	AGT	CAT	TTT	GTC	CAA	AGC									180
K	N	R	S	L	F	D	G	K	L	R	E	M	Q	A	F	F	G	L	T									73
AAG	AAC	AGG	AGT	CTC	TTT	GAT	GGA	AAA	CTT	CGG	GAA	ATG	CAG	GCA	TTT	TTC	GGA	TTG	ACA									240
V	T	G	K	L	D	S	D	T	L	A	I	M	K	V	P	R	C	G	V									133/361
GTG	ACT	GGA	AAA	CTG	GAT	TCA	GAC	ACA	CTT	GCG	ATC	ATG	AAA	GTG	CCC	AGG	TGT	GGG	GTA									93/300
P	D	V	G	Q	Y	G	Y	T	L	P	G	W	R	K	Y	S	L	T	Y									113
CCA	GAT	GTG	GGG	CAA	TAT	GGC	TAC	ACA	CTC	CCT	GGG	TGG	AGA	AAA	TAC	AGC	CTT	ACA	TAC									360
R	I	M	N	Y	T	P	D	M	T	P	A	D	V	D	E	A	I	Q	K									133
AGA	ATA	ATG	AAC	TAT	ACT	CCT	GAT	ATG	ACA	CCA	GCT	GAT	GTG	GAT	GAG	GCT	ATT	CAG	AAA									420
A	L	Q	V	W	S	K	V	T	P	L	T	F	T	R	I	S	K	G	V									153
GCT	CTA	CAA	GTT	TGG	AGC	AAG	GTC	ACT	CCA	CTG	ACG	TTT	ACC	AGG	ATA	TCC	AAG	GGG	GTT									480

Fig. 15F

Table 10

A	D	I	M	I	A	F	R	T	G	V	H	G	W	C	P	R	H	F	D	173
GCA	GAT	ATA	ATG	ATA	GCA	TTC	AGG	ACA	GGA	GTC	CAT	GGC	TGG	TGT	CCT	CGT	CAC	TTT	GAT	540
G	P	L	G	V	L	G	H	A	F	P	P	G	L	G	L	G	G	D	T	193
GGT	CCT	CTG	GGA	GTC	CTT	GGC	CAT	GCC	TTT	CCT	CCT	GGT	CTG	GGT	CTA	GGT	GGT	GAC	ACT	600
H	F	D	E	D	E	T	W	I	A	K	D	G	E	G	F	N	L	F	L	213
CAC	TTT	GAC	GAA	GAT	GAA	ACA	TGG	ATA	GCC	AAG	GAT	GGG	GAA	GGG	TTC	AAC	TTG	TTT	CTT	660
V	A	A	H	E	F	G	H	S	L	G	L	S	H	S	N	D	Q	T	A	233
GTG	GCT	GCT	CAT	GAA	TTT	GGT	CAC	TCT	CTG	GGG	CTG	TCC	CAC	TCC	AAT	GAT	CAA	ACA	GCC	720
L	M	F	P	N	Y	I	S	L	D	P	S	K	Y	P	L	S	Q	D	D	134
TTG	ATG	TTC	CCC	AAT	TAC	ATC	TCC	CTG	GAT	CCT	AGC	AAA	TAC	CCA	CTT	TCT	CAG	GAT	GAT	361
I	D	G	I	Q	S	I	Y	G	S	P	P	K	V	T	T	K	P	S	G	273
ATT	GAT	GGG	ATC	CAG	TCC	ATC	TAT	GGA	AGT	CCA	CCT	AAG	GTA	ACC	ACC	AAG	CCA	AGT	GGA	840
N	S	E	P	H	A	C	D	P	T	L	T	F	D	A	I	T	T	F	R	293
AAT	TCT	GAA	CCC	CAC	GCC	TGT	GAC	CCC	ACC	TTG	ACT	TTT	GAT	GCT	ATC	ACT	ACT	TTC	CGC	900
R	E	V	M	F	F	K	G	R												302
AGG	GAA	GTT	ATG	TTC	TTT	AAA	GGC	AGG												927

Fig. 15G

TAAACCTATTCCTTGACACTCCAGCTTCTTATAAAGATGTTTTTTTTTCAAAGGATCTCCGGATAAACAGTCTTCTA	1007
CTCAGCTAGAAAGCCAGTTGCTGAGCATGTACCAGTACATCAGCAAGAGATTCTTCTCAAGAAACAATGTAGAAAAACAA	1087
TCAAAGAAAACACCCCAAGGCAACCTGCAGCCTCCACACATAAGCACACATGCATTACATGTATGCCCCACATATGTGA	1167
ACATGTAGGCACACATGCATGCATACCACAAAACCTTAAGACTGAAACATGCTGATGGACACACAGGTACCAGGACA	1247
TCATTGATGAAAATATTTTGTGTTTAATGCAGG	1279
H L W R V Y S D I A G A E F E F I D S F	322
CAC TTA TGG AGG GTC TAC TCT GAT ATT GCT GGT GCT GAG TTT GAG TTT ATT GAT TCC TTC	1339
W P S L P A D L Q A A Y E S P R D E L L	342
TGG CCA TCT CTG CCA GCT GAT CTT CAA GCT GCC TAT GAA AGC CCC AGA GAT GAG CTC CTT	1399
V F K D E N F W V I R G Y S V L P G Y P	362
GTT TTT AAA GAT GAG AAT TTC TGG GTC ATC AGG GGA TAT TCT GTC TTG CCC GGT TAC CCC	1459
K S I H T L G F P R R V K K I D A A V C	382
AAA TCC ATC CAC ACA CTC GGA TTT CCA AGA CGT GTG AAG AAA ATT GAT GCA GCC GTC TGT	1519
D H D T R K T F F F V G I W C W R Y D E	402
GAT CAT GAT ACA AGA AAA ACC TTC TTT TTT GTT GGC ATC TGG TGC TGG AGG TAT GAT GAG	1579
M A Q A M D R G G F P Q R I I K C F P G I	422
ATG GCA CAA GCA ATG GAC AGA GGA TTC CCA CAG AGG ATA AAG TGC TTC CCA GGA ATT	1639

Fig. 15H

GenBank

R L R V D A V F Q H N G F L Y F F H G S 442
 CGC CTC CGT GTG GAT GCT GTC TTC CAA CAT AAT GGA TTC CTC TAT TTC TTC CAT GGG TCG 1699

 R Q F E Y D M K A K N I T Q V I K T N S 462
 AGG CAA TTT GAA TAT GAC ATG AAG GCG AAA AAT ATC ACC CAA GTG ATC AAA ACC AAT TCT 1759

 W F L C N E P L N A S F N V S V K G K A 482
 TGG TTC CTG TGT AAC GAA CCA TTA AAC GCA TCA TTC AAT GTC AGT GTC AAA GGA AAA GCA 1819

 N S I G T V I L H H K R L S L L T F S I 502
 AAT TCA ATT GGC ACA GTG ATA TTA CAT CAT AAA AGG TTA AGC TTG CTC ACT TTC AGT ATT 1879

 V H V L T K T Y N * 511
 GTT CAT GTG CTG ACA AAA ACA TAC AAT TAA CAATAAATCCACAATAAACCAAAACAAATCTTTAACC 1949

 TGA ACTCTGCCCTCAGGAAGACTCAAGAGTGGGAGAGATGACCCAGTGGTTAAGTGCACCTGGCTGCTCTTTCAAAGGACCC 2029
 AGGTTTGATTCTCAGTACCCACATGGCAGTCCACAGCTCTCTGTAACCTCAGACCCAGGAAATCTGATGCCCTCTCTGG 2109
 CCTCTGAGGCACTGCACAAAGCATGGTGCATAGACATATACATGCAAGCAACGGCTATATATTAAATAAAATGAAAA 2189
 AGTAAAAATAATTGAGCCCAATTCTTTAGCATCAAGTTCTTACTCCTACTATATATCAGCTGGGTAACCAATAACCAAGTTA 2269
 AAGTATCTGATTCTTCAACAGTGAAGTTTAAATAATGACAAAAATCTCTCACTTATTTTGAGTCTAAATGATTGTC 2349
 AAAC TTGGAAAA TTAAGCATGTCTTAAAAATAAACATTAAAGACAAATCTTAATCCAAAAA AAAAAAAAAAAAAA 2429
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2467

Fig. 15I

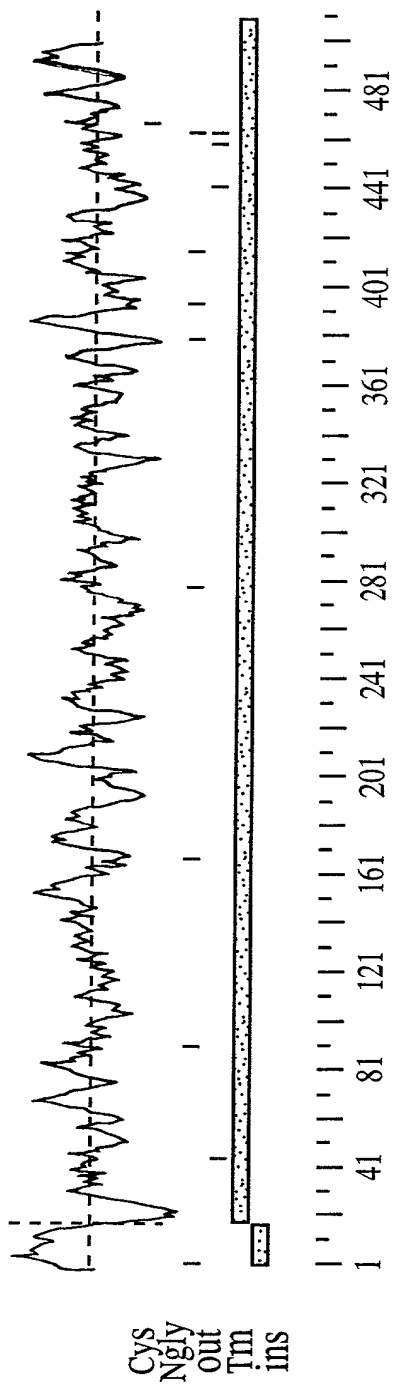


FIG. 15J

Fig. 15L

Figure 15M

```

human  CCGACGCGGTGGCGGACGCGTGGGCAGCTGAAGAAAGAGAGGAATGAAGCGCCTTCTGCTTCTGTTTTT 10 20 30 40 50 60 70
murine  :: : :::::::::: :: :::::::::: :::::::::: :::::::::: :::::::::: :
-----GCTTT-----AACTGAAGA--GACAGGAATGAAGTGCCTTCTGCTCTCTGATGGT
10 20 30 40

human  GTTCTTTATAACATTTTCTCTGCATTTCCCTTAGTCCGGATGACGGAAAATGAAGAAAATATGCAACTG 80 90 100 110 120 130 140
murine  .. :::::::::: :::: :::::::::: :::: :::::::::: :::::::::: :::: ::::::::::
TAAATTTATAACACTTTCGGCTGCATTTCCCTCCAGACAGGAAGGACAAAATGAGGAGAAACAACCAACTG
50 60 70 80 90 100 110

human  GCTCAGGCATATCTCAACCAGTTCCTCTCTGAAATAGAAAGGGAATCATCTTGTTCAAAGCAAGAATA 150 160 170 180 190 200 210
murine  :: :::::::::::::::::::::::::::::::::::::::::::::::::: :::: :::::::::::::::::: :
GCCCAGGCATATCTCAACCAGTTCCTCTCTTGAAATAGAAAGGAGTCATTTGTCCAAAGCAAGAACA
120 130 140 150 160 170 180

human  GGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTGTGATTGACAGTGACTGGAAAACCTGGA 220 230 240 250 260 270 280
murine  :::::::::::::::::: :::: :::::::::::::::::::::::::::::::::: :::::::::::::::::::
GGAGTCTCTTTGATGGAAAACCTTCGGGAAATGCAGGCATTTTTCGGATTGACAGTGACTGGAAAACCTGGA
190 200 210 220 230 240 250

```

Fig. 15M

human	CTCAAACACCCCTTGAGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGCCAGTATGGCTACACC	290	300	310	320	330	340	350
murine	TTCAGACACACTTGGGATCATGAAAGTGCCAGGTGTGGGTACCCAGATGTGGGCAATATGGCTACACA	260	270	280	290	300	310	320
human	CTCCCTGGGTGGAGAAAAATACAACCTCACCTACAGAAATAATAAATACTACTCCGGATATGGCACGAGCTG	360	370	380	390	400	410	420
murine	CTCCCTGGGTGGAGAAAAATACAGCCTTACATACAGAAATAATGAACATACTCTGATATGACACCAGCTG	330	340	350	360	370	380	390
human	CTGTGGATGAGGCTATCCAAGAAAGTTTAGAAGTGTGGAGCAAAGTCACCTCCACTAAATTCACCAAGAT	430	440	450	460	470	480	490
murine	ATGTGGATGAGGCTATTTCAGAAAGCTCTACAAGTTTGAGAGCAAGTCACCTCCACTGACGTTTACCAGGAT	400	410	420	430	440	450	460
human	TTCAAAGGGGATTGCAGACATCATGATTGCCCTTAGGACTCGAGTCCATGGTCGGTGTCTCGCTATTTT	500	510	520	530	540	550	560
murine	ATCCAAGGGGGTTGCAGATATAATGATAGCATTCAGGACAGGAGTCCATGGCTGGTGTCTCGTCACTTT	470	480	490	500	510	520	530

Fig. 15N

Fig. 150

```

840      850      860      870      880      890      900
human  AGGTACCTGCTAAGCCAAAGGAACCCACTATACCCCATGCCCTGTGACCCCTGACTTGACTTTTGACGCTAT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
murine AGGTAACCAACCAAGCCAAGTGGAATTCGAAACCCACGCCCTGTGACCCACCTTGACTTTTGATGCTAT
820      830      840      850      860      870      880

910      920      930      940
human  CACAACCTTCCGCAGAGAAAGTAATGTTCTTTAAAGGCAGG-----
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
murine CACTACTTTCCGCAGGGAAGTTATGTTCTTTAAAGCAGGTAAACCTATTCCCTTGACACTCCAGCTTCT
890      900      910      920      930      940      950

human  -----

murine TATAAAGATGTTTTTTTTTTTCAAAAGGATCTCCGGATAAACAGTCTTCTACTCAGCTAGAAAGCCAGTTG
960      970      980      990      1000      1010      1020

human  -----

murine CTGAGCATGTACCAGTACATCAGCAAGAGATTCTTCCTCAAGAAACAATGTAGAAACAATCAAAGAAAA
1030      1040      1050      1060      1070      1080      1090

```

Fig. 15P

human	1050	1060	1070	1080	1090	1100	1110
	GAAACCCAGAGATAAGATTCTGGTTTTTAAAGATGAAAACTTCTGGATGATCAGAGGATAATGCTCTTG						
murine	1380	1390	1400	1410	1420	1430	1440
	AAGCCCCAGAGATGAGCTCCTTGTTTTAAAGATGAGAAATTTCTGGGTGATCAGGGGATATTTCTGTCTTG						
human	1120	1130	1140	1150	1160	1170	1180
	CCAGATTATCCCAAATCCATCCATACATTAGGTTTCCAGGACGTGTGAAGAAAATAGATGCAGCCGCTCT						
murine	1450	1460	1470	1480	1490	1500	1510
	CCCGGTTACCCCAAATCCATCCACACACTCGGATTTCCAAGACGTGTGAAGAAAATTTGATGCAGCCGCTCT						
human	1190	1200	1210	1220	1230	1240	1250
	GTGATAAGACCACAAGAAAAACCTACTTCTTTGTGGGCATTTGGTGCTGGAGGTTTGATGAAATGACCCA						
murine	1520	1530	1540	1550	1560	1570	1580
	GTGATCATGATACAAGAAAAACCTTCTTTTGTGGCATCTGGTGCTGGAGGTATGATGAGATGGCACA						
human	1260	1270	1280	1290	1300	1310	1320
	AACCATGGACAAAGGATTCCCGCAGAGAGTGGTAAAAACACTTTCCTGGAATCAGTATCCGTGTGATGCT						
murine	1590	1600	1610	1620	1630	1640	1650
	AGCAATGGACAGAGGATTCCACAGAGGATAATAAAGTGCTTCCAGGAATTCGCCCTCCGTGTGATGCT						

Fig. 15R

```

950
human  -----
murine CACCCAAGGGCAACCTGCAGCCTCCACACATAAGCACACATGCATTTCACATGTATGCCCCACATATGTGA
1100      1110      1120      1130      1140      1150      1160

human  -----
murine ACATGTAGGCACACATGCATGCATACCAAAACCACAAACTTAAGACTGAAACATGCTGATGGACACAGG
1170      1180      1190      1200      1210      1220      1230

human  -----
          960      970
          -----CACCTATGGAGGATCTATTATGATATCA
          ::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
murine TACCAGGACATCATTTGATGAAATAATTTTGTGTTTAATGCAGGCACCTTATGGAGGGTCTACTCTGATATTG
1240      1250      1260      1270      1280      1290      1300

          980      990      1000      1010      1020      1030      1040
human  CGGATGTTGAGTTTGAATTGCTTCATCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
murine CTGGTGCTGAGTTTGAGTTTATGATTCCTTCTGGCCATCTCTGCCAGCTGATCTTCAAGCTGCCTATGA
1310      1320      1330      1340      1350      1360      1370

```

Fig. 15Q

Fig. 15T

```

1670
human  TAACAACAA-----
      ::::::::::
murine TAGCATCAAGTTCTTACTCCTACTATATACAGCTGGGTAACCAATAACCAGTTAAAGTATCTGATTCTTT
      2220  2230  2240  2250  2260  2270  2280

human  -----

murine CTAACAGTGAAGTTTAAATATGACAAAAATCTCTCACTTATTTTGAGTCTAATTAATGATTGCAAACT
      2290  2300  2310  2320  2330  2340  2350

human  -----

murine TGGAAAATTAAAGCATGTCTTAAAAATAAACATTAAAGACAAATTCTTAATCCAAAAAATAAAAAA
      2360  2370  2380  2390  2400  2410  2420

human  -----1680
      -----AAAAAATAAAAAA
      ::::::::::::::
murine AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
      2430  2440  2450  2460
```

Fig. 15U

Fig. 15V

[illegible]

Fig. 15W

```

10      20      30      40      50      60
210 ATGAAGCGCCTTCT---GCTTCTGTTTTTGTCTTTTATAACATTTTCT-TCTGCAATTCCCTTAGTCCG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 ATGTT-CTCCCTGAAGACGCTTCCATTTCTGCTCTTACTC-CATGTGCAGATTTCCAAAGGCCTT--TCCT
      10      20      30      40      50      60

70      80      90      100     110     120     130
210 GATGACGGAATGAAGAAAATA-TGCAACTGGCTCAGGCATATCTCAACCAGTTCTACTCTCTTGAAT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 G-TATCTTCTAAAGAGAAAAATACAAAAACTGT-TCAGGACTACCTGGAAAAGTTCTAC-CAATTACCAA
      70      80      90      100     110     120     130

140     150     160     170     180     190     200
210 AGAAG-GGAATCATCTTGTTCAAAGCAAGAATAG--GAGTCTCATAGATGACAAAATTCGGGAAATGCA
      . : . : . : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 GCAACCAGTATCAG--TCTACAAGG-AAGAAATGGCACTAATGTGATCGTTGAAAAGCTTAAAGAAATGCA
      140     150     160     170     180     190     200

210     220     230     240     250     260     270
210 AGCATTTTTTGGATTGACAGTGACTGGAAAACTGGACTCAAACACCCTTGAGATCATGAAGACACCCAGG
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 GCGATTTTTTGGTTGAATGTGACGGGGAAGCCAAATGAGGAAACTCTGGACATGATGAAAAAGCCTCGC
      210     220     230     240     250     260     270

```

Fig. 15X-1

Fig. 15X-2

Fig. 15X-3

Fig. 15X-4

```

1100      1110      1120      1130      1140      1150      1160
210 TAGGTTTCCAGGACGTGTGAAGAAATAGATGCAGCCGTCGTGATAAGACCAAGAAAAACCTACTT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 ATGGCTTCCCAGCAGCGTCCAAGCAATTGACGCAGC-----TGTTTTCTACAGAAGTAAACATACTT
      1110      1120      1130      1140      1150      1160

1170      1180      1190      1200      1210      1220      1230
210 CTTTGTGGGCATTGTGTCTGGAGGTTTGATGAAATGACCCAAACCATGGACAAAGGATTCCCGCAGAGA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 CTTTGTAAATGACCAATTTCTGGAGATATGAT-----AACCAAAGACAAATT-----CATGGAGC
      1170      1180      1190      1200      1210

1240      1250      1260      1270      1280      1290      1300
210 GTGGTAAACACTTTCCTGGAATCAGTATCCGTGTGATGCTGCTTCCAGTACAAAGGATTCTTCTTTT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 CAGGT-----TATCCCAAAGCA-TATC-----AGGTGC--CTTTCAGGAATAGAGAGTAA-----
      1220      1230      1240      1250      1260

1310      1320      1330      1340      1350      1360      1370
210 TCAGCCGTGGATCAAAGCAATTTGAATACAACATTAAAGACAAAGAATATTACCCGAATCATGAGAACTAA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 -----GTTGAT----GCAGTTT---TCCAGCA-----AGAACATTTC---TTC-----
      1270      1280      1290      1300

```

Fig. 15X-5

```

1380      1390      1400      1410      1420      1430      1440
210 TACTTGTTTCAATGCAAGAACCAAGAACTCCTCATTTGGTTTGTGATATCAACAAGGAAAAGCACAT
      :.: : : :.:.:.:.:.: : :.:.:.:.:.: : :.:.:.:.:.: :
MMP-8 --CATG----TC--TTCAGTGGACCAAGATATTACGCATTTGATCTT-ATTGCT-CAGAGAGTTA-C-----
      1310      1320      1330      1340      1350

1450      1460      1470      1480      1490      1500      1510
210 TCAGGAGGCATAAAGATATTGTATCATAAAGAGTTTAAGCTTGTTTATTTTGGTATTGTTCAATTGCTGA
      :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
MMP-8 -CAGA-----GTTGCAAGAG-----GCA-----ATAAATGG-----C-TTAACTGT
      1360      1370      1380      1390

1520      1530
210 AAAACACTTCTATTATCAA
      :.: :.: :.: :
MMP-8 AGA-----TATGGC--
      1400

```

Fig. 15X-6

GAAAAGCGCTGCGGAGGGCCCGGGCCCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCC 79
 M P P W P L L L L L L A V S G A Q T T R 18
 CCCACC ATG CCG TGG CCC CTG CTG CTG CTG GGC GTG AGT GGG GCC CAG ACA ACC CGG 139
 P C F P G C Q C E V E T F G L F D S F S 38
 CCA TGC TTC CCC GGG TGC CAA TGC GAG GTG GAG ACC TTC GGC CTT TTC GAC AGC TTC AGC 199
 L T R V D C S G L G P H I M P V P I P L 58
 CTG ACT CGG GTG GAT TGT AGC GGC CTG GGC CCC CAC ATC ATG CCG GTG CCC ATC CCT CTG 259
 D T A H L D L S S N R L E M V N E S V L 78
 GAC ACA GCC CAC TTG GAC CTG TCC AAC CGG CTG GAG ATG GTG AAT GAG TCG GTG TTG 319
 A G P G Y T T L A G L D L S H N L L T S 98
 GCG GGG CCG GGC TAC ACG ACG TTG GCT GGC CTG GAT CTC AGC CAC AAC CTG CTC ACC AGC 379
 I S P T A F S R L R Y L E S L D L S H N 118
 ATC TCA CCC ACT GCC TTC TCC CGC CTT CGC TAC CTG GAG TCG CTT GAC CTC AGC CAC AAT 439
 G L T A L P A E S F T S S P L S D V N L 138
 GGC CTG ACA GCC CTG CCA GCC GAG AGC TTC ACC AGC TCA CCC CTG AGC GAC GTG AAC CTT 499

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Fig. 16A

S H N Q L R E V S S V S A F T T H S Q G R 158
 AGC CAC AAC CAG CTC CGG GAG GTC TCA GTG TCT GCC TTC ACG ACG CAC AGT CAG GGC CGG 559

A L H V D L S H N L I H R L V P H P T R 178
 GCA CTA CAC GTG GAC CTC TCC CAC AAC CTC ATT CAC CGC CTC GTG CCC CAC CCC ACG AGG 619

A G L P A P T I Q S L N L A W N R L H A 198
 GCC GGC CTG CCT GCG CCC ACC ATT CAG AGC CTG AAC CTG GCC TGG AAC CGG CTC CAT GCC 679

V P N L R D L P L R Y L S L D G N P L A 218
 GTG CCC AAC CTC CGA GAC TTG CCC CTG CGC TAC CTG AGC CTG GAT GGG AAC CCT CTA GCT 739

V I G P G A F A G L G G L T H L S L A S 238
 GTC ATT GGT CCG GGT GCC TTC GCG GGG CTG GGA GGC CTT ACA CAC CTG TCT CTG GCC AGC 799

L Q R L P E L A P S G F R E L P G L Q V 258
 CTG CAG AGG CTC CCT GAG CTG GCG CCC AGT GGC TTC CGT GAG CTA CCG GGC CTG CAG GTC 859

L D L S G N P K L N W A G A E V F S G L 278
 CTG GAC CTG TCG GGC AAC CCC AAG CTT AAC TGG GCA GGA GCT GAG GTG TTT TCA GGC CTG 919

S S L Q E L D L S G T N L V P L P E A L 298
 AGC TCC CTG CAG GAG CTG GAC CTT TCG GGC ACC AAC CTG GTG CCC CTG CCT GAG GCG CTG 979

Fig. 16B

L L H L P A L Q S V S V G Q D V R C R R 318
 CTC CTC CAC CTC CCG GCA CTG CAG AGC GTC AGC GTG GGC CAG GAT GTG CGG TGC CGG CGC 1039

 L V R E G T Y P R R P G S S P K V A L H 338
 CTG GTG CGG GAG GGC ACC TAC CCC CGG AGG CCT GGC TCC AGC CCC AAG GTG GCC CTG CAC 1099

 C V D T R E S A A R G P T I L * 354
 TGC GTA GAC ACC CGG GAA TCT GCT GCC AGG GGC CCC ACC ATC TTG TGA 1147

 CAAATGGTGTGCCCCAGGGCCACATAACAGACTGCTGTCTGGGTGCTCCAGGTCCCGAGTAACTTATGTTCAATGTG 1226
 CCAACACAGGGGGAGCCCGCAGGCCTATGTGGCAGCGTCACCAACAGAGATTGTGGCCCTAGGAGAGGCTTTTGACCT 1305
 GGGAGCCACACCTAGGAGCAAGTCTACCCCTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGACATTCGATGC 1384
 CAAACCAGACTCGGGTCCCCCTCCTGCTTCCCTTCCCAAGTGCCCTTCCCTCATGCTGGCCGCGCTG 1463
 ACCCGCAATGGCAGAGGGTGGGTGGGACCCCCCTGCTGCAGGCGAGATTCAAGTCCACCCCTTCTCATGTGACAGAT 1542
 GCCCATGGCCAGTCACTCAGGGCGAGTTTCTTTCTAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCCGCTT 1621
 CATCCTTTTCTATTCCCTAGAAACCTTAATGGTAGAAGGAATTGCAAGAATCAAGTCCACCCCTTCTCATGTGACAGAT 1700
 GGGGAAACTGAGGCCCTTGAGAAAGGAAAGGCTAATCTAAGTTCTGCGGCGAGTGGCATGACTGGAGCACAGCCCTCCT 1779
 GCCTCCAGCCCGACCAATGCACCTTCTTGTCTCTCTAATAAGCCCCACCTCCCGCCCTGGGCTCCCTTGCTGC 1858
 CCTTGCCCTGTTCCCATTAGCACAGGAGTAGCAGCAGCAGGACAGGCAAGAGCCCTCAAGTGGGACTCTGGGCCCTCTG 1937
 ACCAGCTGTGCGGCATGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCACATTTGGTTCCAGCCCTAGC 2016
 CAGTTTCTCACCCCTGGGTGGGTCCCCCAGCATCCAGACTGGAACCTACCCATTTTCCCTGAGCATCCTCTAGATG 2095
 CTGCCCAAGGAGTTGCTGCAGTTCTGAGCCCTCATCTGGCTGGGATCTCCAAGGGCCCTCCTGGATTCAAGTCCCCACT 2174
 GGCCCTGAGCACGACAGCCCTTCTTACCCCTCCAGGAATGCCGTGAAGGAGACAAGGTCTGCCCGACCCCATGTCTATG 2253

Fig. 16C

CTCTACCCAGGGCAGCATCTCAGCTTCCGAACCCCTGGGCTGTTCCCTTAGTCTTCAATTTATAAAAGTTGTTCCTT 2332
 TTTAACGGAGTGTCACTTTCAACCGGCTCCCCCTACCCCTGCTGCCGGGATGGAGACATGTCATTTGTAAAAGCAGA 2411
 AAAAGGTTGCATTTGTTCACTTTTGTAAATATTGTCCCTGGCCCTGTGTTGGGGTGTGGGGAAGCTGGGCATCAGTGGC 2490
 CACATGGGCATCAGGGGCTGGCCCAACAGAGACCCCAACAGGCGAGTGAAGCTCTGTCTTCCCCCACCTGCTAGCCCATC 2569
 ATCTATCTAACCGGTCCCTTGATTTAATAAACACTATAAAAGTTAAAAAATAAAAAA 2628

Fig. 16D

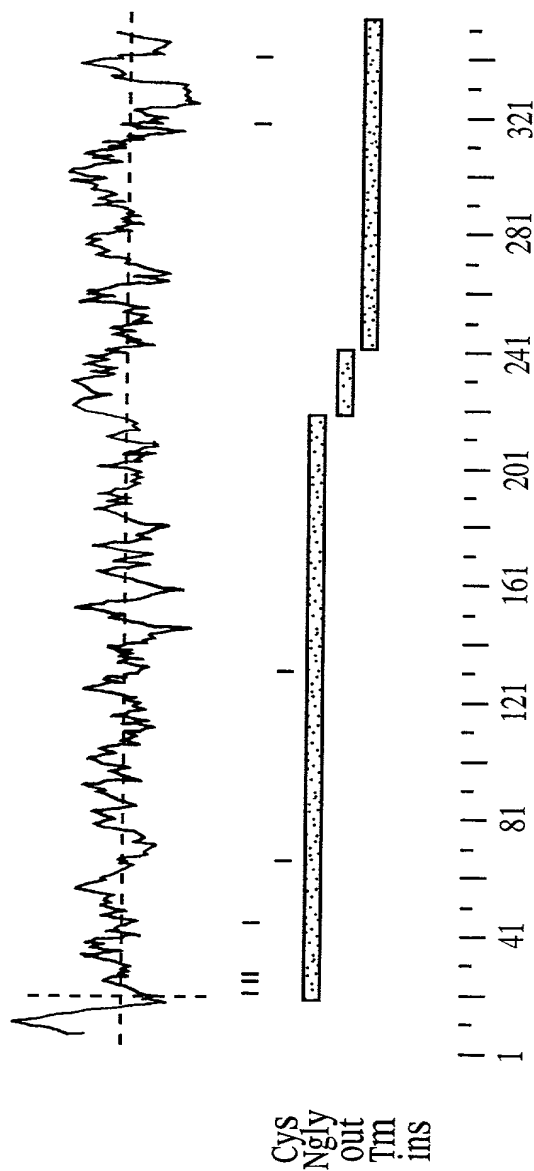


FIG. 16E

GTCGACCCACGCTCCGCCCGGCTAGCGCCGGTCCGCCGAGCCGAGCCGAGCGGCGGAGCCTC	79
TGGAATCACCCGGGTCGCTGTTCTGAGGTGGTCAAGGTGGACAGGGCGGTGATGCGCAGTTTGACACTGAAT	158
ACCAGCGCTAGAGGCCTCCTATAGTATTACACCCCGAGGGAGGACCTGTTGGTGCACGTCGCCGAGGGAGCAA	237
GTCACCTTGGCACCATATTGAACCTTGACCTCTTCTCTCGAGTTTATAATCTGCACCAAGAATGGCTTCACA	316
M L I G E I F E L M Q F L F V V A F T	19
TGT ATG CTC ATC GGG GAG ATC TTT GAG CTC ATG CAG TTC CTC TTT GTG GTT GCC TTC ACT	376
T F L V S C V D Y D I L F A N K M V N H	39
ACC TTC CTG GTC AGC TGC GTG GAC TAT GAC ATC CTA TTT GCC AAC AAG ATG GTG AAC CAC	436
S L H P T E P V K V T L P D A F L P A Q	59
AGT CTT CAC CCT ACT GAA CCC GTC AAG GTC ACT CTG CCA GAC GCC TTT TTG CCT GCT CAA	496
V C S A R I Q E N G S L I T I L V I A G	79
GTC TGT AGT GCC AGG ATT CAG GAA AAT GGC TCC CTT ATC ACC ATC CTG GTC ATT GCT GGT	556
V F W I H R L I K F I Y N I C C Y W E I	99
GTC TTC TGG ATC CAC CGG CTT ATC AAG TTC ATC TAT AAC ATT TGC TGC TAC TGG GAG ATC	616
H S F Y L H A L R I P M S A L P Y C T W	119
CAC TCC TTC TAC CTG CAC GCT CTG CGC ATC CCT ATG TCT GCC CTT CCG TAT TGC ACG TGG	676

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Fig. 17A

Q	E	V	Q	A	R	I	V	Q	T	Q	K	E	H	Q	I	C	I	H	K	139
CAA	GAA	GTG	CAG	GCC	CGG	ATC	GTG	CAG	ACG	CAG	AAG	GAG	CAC	CAG	ATC	TGC	ATC	CAC	AAA	736
R	E	L	T	E	L	D	I	Y	H	R	I	L	R	F	Q	N	Y	M	V	159
CGT	GAG	CTG	ACA	GAA	CTG	GAC	ATC	TAC	CAC	CGC	ATC	CTC	CGT	TTC	CAG	AAC	TAC	ATG	GTG	796
A	L	V	N	K	S	L	L	P	L	R	F	R	L	P	G	L	G	E	A	179
GCA	CTG	GTT	AAC	AAA	TCC	CTC	CTG	CCT	CTG	CGC	TTC	CGC	CTG	CCT	GGC	CTC	GGG	GAA	GCT	856
V	F	F	T	R	G	L	K	Y	N	F	E	L	I	L	F	W	G	P	G	199
GTC	TTC	TTC	ACC	CGT	GGT	CTC	AAG	TAC	AAC	TTT	GAG	CTG	ATC	CTC	TTC	TGG	GGA	CCT	GGC	916
S	L	F	L	N	E	W	S	L	K	A	E	Y	K	R	G	G	Q	R	L	219
TCT	CTG	TTT	CTC	AAT	GAA	TGG	AGC	CTC	AAG	GCC	GAG	TAC	AAA	CGT	GGG	GGG	CAA	CGG	CTA	976
E	L	A	Q	R	L	S	N	R	I	L	W	I	G	I	A	N	F	L	L	239
GAG	CTG	GCC	CAG	CGC	CTC	AGC	AAC	CGC	ATC	CTG	TGG	ATT	GGC	ATC	GCT	AAC	TTC	CTG	CTG	1036
C	P	L	I	L	I	W	Q	I	L	Y	A	F	F	S	Y	A	E	V	L	259
TGC	CCC	CTC	ATC	CTC	ATA	TGG	CAA	ATC	CTC	TAT	GCC	TTC	TTC	AGC	TAT	GCT	GAG	GTG	CTG	1096
K	R	E	P	G	A	L	G	A	R	C	W	S	L	Y	G	R	C	Y	L	279
AAG	CGG	GAG	CCG	GGG	GCC	CTG	GGA	GCA	CGC	TGC	TGG	TCA	CTC	TAT	GGC	CGC	TGC	TAC	CTC	1156

Fig. 17B

R H F N E L E H E L E L Q S R L N R G Y K P 299
 CGC CAC TTC AAC GAG CTG GAG CAC GAG CTG CAG TCC CGC CTC AAC CGT GGC TAC AAG CCC 1216

A S K Y M N C F L S P L L T L A K N G 319
 GCC TCC AAG TAC ATG AAT TGC TTC TTG TCA CCT CTT TTG ACA CTG CTG GCC AAG AAT GGA 1276

A F F A G S I L A V L I A L T I Y D E D 339
 GCC TTC TTC GCT GGC TCC ATC CTG GCT GTG CTT ATT GCC CTC ACC ATT TAT GAC GAA GAT 1336

V L A V E H V L T T V T L L G V T V T V 359
 GTG TTG GCT GTG GAA CAT GTG CTG ACC ACC GTG ACA CTC CTG GGC GTC ACC GTG ACC GTG 1396

C R S F I P D Q H M V F C P E Q L L R V 379
 TGC AGG TCC TTT ATC CCG GAC CAG CAC ATG GTG TTC TGC CCT GAG CAG CTG CTC CGC GTG 1456

I L A H I H Y M P D H W Q G N A H R S Q 399
 ATC CTC GCT CAC ATC CAC TAC ATG CCT GAC CAC TGG CAG GGT AAT GCC CAC CGC TCG CAG 1516

T R D E F A Q L F Q Y K A V F I L E E L 419
 ACC CGG GAC GAG TTT GCC CAG CTC TTC CAG TAC AAG GCA GTG TTC ATT TTG GAA GAG TTG 1576

L S P I V T P L I L I F C L R P R A L E 439
 CTG AGC CCC ATT GTC ACA CCC CTC ATC CTC ATC TTC TGC CTG CGC CCA CGG GCC CTG GAG 1636

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Fig. 17C

I I D F F R N F T V E V V G V G D T C S 459
 ATT ATA GAC TTC TTC CGA AAC TTC ACC GTG GAG GTC GTT GGT GTG GGA GAT ACC TGC TCC 1696

 F A Q M D V R Q H G H P Q W L S A G Q T 479
 TTT GCT CAG ATG GAT GAT GTT CGC CAG CAT GGT CAT CCC CAG TGG CTA TCT GCT GGG CAG ACA 1756

 E A S V Y Q Q A E D G K T E L S L M H F 499
 GAG GCC TCA GTG TAC CAG CAG CAA GCT GAG GAT GGA AAG ACA GAG TTG TCA CTC ATG CAC TTT 1816

 A I T N P G W Q P P R E S T A F L G L 519
 GCC ATC ACC AAC CCT GGC TGG CAG CCA CCA GAT GAG AGC ACA GCC TTC CTA GGC TTC CTC 1876

 K E Q V Q R D G A A S L A Q G G L L P 539
 AAG GAG CAG GTT CAG CGG GAT GGA GCA GCT GCT AGC CTC GCC CAA GGG GGT CTG CTC CCT 1936

 E N A L F T S I Q S L Q S E S E P L S L 559
 GAA AAT GCC CTC TTT ACG TCT ATC CAG TCC TTA CAA TCT GAG TCT GAG CCC CTG AGC CTT 1996

 I A N V V A G S S C R G P P L P R D L Q 579
 ATC GCA AAT GTG GTA GCT GGC TCA TCC TGC CGG GGC CCT CCA CTG CCC AGA GAC CTG CAG 2056

 G S R H R A E V A S A L R S F S P L Q P 599
 GGC TCC AGG CAC AGG GCT GAA GTC GCC TCT GCC CTG CGC TCC TTC TCC CCG CTG CAA CCC 2116

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Fig. 17D

Fig. 17E

[illegible]

Fig. 17F

[illegible]

Fig. 17H

G	S	L	I	T	I	L	V	I	A	G	V	F	W	I	H	R	L	I	K	149
GGC	TCC	CTT	ATC	ACC	ATC	CTG	GTC	ATT	GCT	GGT	GTC	TTC	TGG	ATC	CAC	CGG	CTT	ATC	AAG	566
F	I	Y	N	I	C	C	Y	W	E	I	H	S	F	Y	L	H	A	L	R	169
TTC	ATC	TAT	AAC	ATT	TGC	TGC	TAC	TGG	GAG	ATC	CAC	TCC	TTC	TAC	CTG	CAC	GCT	CTG	CGC	626
I	P	M	S	A	L	P	Y	C	T	W	Q	E	V	Q	A	R	I	V	Q	189
ATC	CCT	ATG	TCT	GCC	CTT	CCG	TAT	TGC	ACG	TGG	CAA	GAA	GTG	CAG	GCC	CGG	ATC	GTG	CAG	686
T	Q	K	E	H	Q	I	C	I	H	K	R	E	L	T	E	L	D	I	Y	209
ACG	CAG	AAG	GAG	CAC	CAG	ATC	TGC	ATC	CAC	AAA	CGT	GAG	CTG	ACA	GAA	CTG	GAC	ATC	TAC	746
H	R	I	L	R	F	Q	N	Y	M	V	A	L	V	N	K	S	L	L	P	229
CAC	CGC	ATC	CTC	CGT	TTC	CAG	AAC	TAC	ATG	GTG	GCA	CTG	GTT	AAC	AAA	TCC	CTC	CTG	CCT	806
L	R	F	R	L	P	G	L	G	E	A	V	F	F	T	R	G	L	K	Y	249
CTG	CGC	TTC	CGC	CTG	CCT	GGC	CTC	GGG	GAA	GCT	GTC	TTC	TTC	ACC	CGT	GGT	CTC	AAG	TAC	866
N	F	E	L	I	L	F	W	G	P	G	S	L	F	L	N	E	W	S	L	269
AAC	TTT	GAG	CTG	ATC	CTC	TTC	TGG	GGA	CCT	GGC	TCT	CTG	TTT	CTC	AAT	GAA	TGG	AGC	CTC	926
K	A	E	Y	K	R	G	G	Q	R	L	E	L	A	Q	R	L	S	N	R	289
AAG	GCC	GAG	TAC	AAA	CGT	GGG	GGG	CAA	CGG	CTA	GAG	CTG	GCC	CAG	CGC	CTC	AGC	AAC	CGC	986

Fig. 17I

I	L	W	I	I	G	I	A	N	F	L	L	C	P	L	I	L	I	W	Q	I	309
ATC	CTG	TGG	ATT	GGC	ATC	GCT	AAC	TTC	CTG	CTG	CTG	TGC	CCC	CTC	ATC	CTC	ATA	TGG	CAA	ATC	1046
L	Y	A	F	F	S	Y	A	E	V	L	L	K	R	E	P	G	A	L	G	A	329
CTC	TAT	GCC	TTC	TTC	AGC	TAT	GCT	GAG	GTG	CTG	CTG	AAG	CGG	GAG	CCG	GGG	GCC	CTG	GGA	GCA	1106
R	C	W	S	L	Y	G	R	C	Y	L	L	R	H	F	N	E	L	E	H	E	349
CGC	TGC	TGG	TCA	CTC	TAT	GGC	CGC	TGC	TAC	CTC	CTC	CGC	CAC	TTC	AAC	GAG	CTG	GAG	CAC	GAG	1166
L	Q	S	R	L	N	R	G	Y	K	P	A	S	K	Y	M	N	C	F	L		369
CTG	CAG	TCC	CGC	CTC	AAC	CGT	GGC	TAC	AAG	CCC	GCC	TCC	TCC	AAG	TAC	ATG	AAT	TGC	TTC	TTG	1226
S	P	L	L	T	L	L	A	K	N	G	A	F	F	A	A	G	S	I	L	A	171/361
TCA	CCT	CTT	TTG	ACA	CTG	CTG	GCC	AAG	AAT	GGA	GCC	TTC	TTC	TTC	GCT	GGC	TCC	ATC	CTG	GCT	389
V	L	I	A	L	T	I	Y	D	E	D	V	L	L	A	V	E	H	V	L	T	409
GTG	CTT	ATT	GCC	CTC	ACC	ATT	TAT	GAC	GAA	GAT	GTG	TTG	GCT	GTG	GAA	CAT	GTG	CTG	ACC	1346	
T	V	T	L	L	G	V	T	V	T	V	C	R	S	F	I	P	D	Q	H		429
ACC	GTC	ACA	CTC	CTG	GGG	GTC	ACC	GTG	ACC	GTG	TGC	AGG	TCC	TTT	ATC	CCG	GAC	CAG	CAC	1406	
M	V	F	C	P	E	Q	L	L	R	V	I	L	A	H	I	H	Y	M	P		449
ATG	GTG	TTC	TGC	CCT	GAG	CAG	CTG	CTC	CGC	GTG	ATC	CTC	GCT	CAC	ATC	CAC	TAC	ATG	CCT	1466	

Fig. 17J

D	H	W	Q	G	N	A	H	R	S	Q	T	R	D	E	F	A	Q	L	F	469
GAC	CAC	TGG	CAG	GGT	AAT	GCC	CAC	CGC	TCG	CAG	ACC	CGG	GAC	GAG	TTT	GCC	CAG	CTC	TTC	1526
Q	Y	K	A	V	F	I	L	E	E	L	L	S	P	I	V	T	P	L	I	489
CAG	TAC	AAG	GCA	GTG	TTC	ATT	TTG	GAA	GAG	TTG	CTG	AGC	CCC	ATT	GTC	ACA	CCC	CTC	ATC	1586
L	I	F	C	L	R	P	R	A	L	E	I	I	D	F	F	R	N	F	T	509
CTC	ATC	TTC	TGC	CTG	CGC	CCA	CGG	GCC	CTG	GAG	ATT	ATA	GAC	TTC	TTC	CGA	AAC	TTC	ACC	1646
V	E	V	V	G	V	G	D	T	C	S	F	A	Q	M	D	V	R	Q	H	529
GTG	GAG	GTC	GTT	GGT	GTG	GGA	GAT	ACC	TGC	TCC	TTT	GCT	CAG	ATG	GAT	GTT	CGC	CAG	CAT	1706
G	H	P	Q	W	L	S	A	G	Q	T	E	A	S	V	Y	Q	Q	A	E	549
GGT	CAT	CCC	CAG	TGG	CTA	TCT	GCT	GGG	CAG	ACA	GAG	GCC	TCA	GTG	TAC	CAG	CAA	GCT	GAG	1766
D	G	K	T	E	L	S	L	M	H	F	A	I	T	N	P	G	W	Q	P	569
GAT	GGA	AAG	ACA	GAG	TTG	TCA	CTC	ATG	CAC	TTT	GCC	ATC	ACC	AAC	CCT	GGC	TGG	CAG	CCA	1826
P	R	E	S	T	A	F	L	G	F	L	K	E	Q	V	Q	R	D	G	A	589
CCA	CGT	GAG	AGC	ACA	GCC	TTC	CTA	GGC	TTT	CTC	AAG	GAG	CAG	GTT	CAG	CGG	GAT	GGA	GCA	1886
A	A	S	L	A	Q	G	G	L	L	P	E	N	A	L	F	T	S	I	Q	609
GCT	GCT	AGC	CTC	GCC	CAA	GGG	GGT	CTG	CTC	CCT	GAA	AAT	GCC	CTC	TTT	ACG	TCT	ATC	CAG	1946

Fig. 17K

S	L	Q	S	E	S	E	P	L	S	L	I	A	N	V	A	G	S	S	629
TCC	TTA	CAA	TCT	GAG	TCT	GAG	CCC	CTG	AGC	CTT	ATC	GCA	AAT	GTG	GTA	GCT	TCA	TCC	2006
C	R	G	P	P	L	P	R	D	L	Q	G	S	R	R	A	H	S	T	649
TGC	CGG	GGC	CCT	CCA	CTG	CCC	AGA	GAC	CTG	CAG	GGC	TCC	AGG	CGG	GCT	CAC	AGC	ATG	2066
T	G	S	G	V	D	A	R	T	A	S	S	G	S	S	V	W	E	G	669
ACA	GGC	TCT	GGG	GTG	GAT	GCC	AGG	ACA	GCC	AGC	TCC	GGG	AGC	AGC	GTG	TGG	GAA	GGA	2126
L	Q	S	L	V	L	S	E	Y	A	S	T	E	M	S	L	H	A	L	689
CTG	CAG	AGC	CTG	GTG	CTG	TCA	GAA	TAT	GCA	TCC	ACA	GAG	ATG	AGC	CTG	CAT	GCC	CTC	2186
M	H	Q	L	H	K	Q	Q	A	Q	A	E	P	E	R	H	V	W	H	709
ATG	CAC	CAG	CTC	CAC	AAG	CAG	CAG	GCC	CAG	GCT	GAA	CCT	GAG	CGG	CAT	GTA	TGG	CAC	2246
R	E	S	D	E	S	G	E	S	A	P	D	E	G	G	E	G	A	R	729
CGG	GAG	AGT	GAT	GAG	AGT	GGA	GAA	AGC	GCC	CCT	GAT	GAA	GGG	GGA	GAG	GCC	CGG	GCC	2306
P	Q	S	I	P	R	S	A	S	Y	P	C	A	A	P	R	P	G	A	749
CCC	CAG	TCT	ATC	CCT	CGC	TCT	GCT	AGC	TAT	CCC	TGT	GCA	GCA	CCC	CGG	CCT	GGA	GCT	2366
E	T	T	A	L	H	G	G	F	Q	R	R	Y	G	G	I	T	D	P	769
GAG	ACC	ACC	GCC	CTG	CAT	GGG	GGC	TTC	CAG	AGG	CGC	TAC	GGT	GGC	ATC	ACA	GAT	CCT	2426

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Fig. 17L

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Fig. 17M

Fig. 17M

GCTGGAGCGGAGCGCAGGCAATGCTCAGCCCTGGATGTAGCTGAGAGGCTGGGAGAAGACGACCGCTGGAGACCG 79
AGCGCGTGGGGAAGACCTAGGGGGTGGTGGGGAAGCAGACAGGAGAACAACCTCGAAATCAAGCGCTTACAGATTA 158

TTTTATTTTGTATAGAGAACACGTAGCGACTCCGAAGATCAGCCCCA ATG AAC ATG TCA GTG TTG ACT TTA 8
229

Q E Y E F E K Q F N E N E A I Q W M Q E 28
CAA GAA TAT GAA TTC GAA AAG CAG TTC AAC GAG AAT GAA GCC ATC CAA TGG ATG CAG GAA 289

N W K K S F L F S A L Y A A F I F G G R 48
AAC TGG AAG AAA TCT TTC CTG TTT TCT GCT GCT TAT GCT GCC TTT ATA TTC GGT GGT CGG 349

H L M N K R A K F E L R K P L V L W S L 68
CAC CTA ATG AAT AAA CGA GCA AAG TTT GAA CTG AGG AAG CCA TTA GTG CTC TGG TCT CTG 409

T L A V F S I F G A L R T G A Y M V Y I 88
ACC CTT GCA GTC TTC AGT ATA TTC GGT GCT CTT CGA ACT GGT GCT TAT ATG GTG TAC ATT 469

L M T K G L K Q S V C D Q G F Y N G P V 108
TTG ATG ACC AAA GGC CTG AAG CAG TCA GTT TGT GAC CAG GGT TTT TAC AAT GGA CCT GTC 529

S K F W A Y A F V L S K A P E L G D T I 128
AGC AAA TTC TGG GCT TAT GCA TTT GTG CTA AGC AAA GCA CCC GAA CTA GGA GAT ACA ATA 589

Fig. 18A

F I I L R K Q K L I F L H W Y H H I T V 148
 TTC ATT ATT CTG AGG AAG CAG AAG CTG ATC TTC CTG CAC TGG TAT CAC CAC ATC ACT GTG 649

 L L Y S W Y S Y K D M V A G G W F M T 168
 CTC CTG TAC TCT TGG TAC TCC TAC AAA GAC ATG GTT GCC GGA GGT TGG TTC ATG ACT 709

 M N Y G V H A V M Y S Y Y A L R A A G F 188
 ATG AAC TAT GGC GTG CAC GCC GTG ATG TAC TCT TAC TAT GCC TTG CGG GCG GCA GGT TTC 769

 R V S R K F A M F I T L S Q I T Q M L M 208
 CGA GTC TCC CGG AAG TTT GCC ATG TTC ATC ACC TTG TCC CAG ATC ACT CAG ATG CTG ATG 829

 G C V V N Y L V F C W M Q H D Q C H S H 228
 GGC TGT GTG GTT AAC TAC CTG GTC TTC TGC TGG ATG CAG CAT GAC CAG TGT CAC TCT CAC 889

 F Q N I F W S S L M Y L S Y L V L F C H 248
 TTT CAG AAC ATC TTC TGG TCC TCA CTC ATG TAC CTC AGC TAC CTT GTG CTC TTC TGC CAT 949

 F F F E A Y I G K M R K T T K A E * 266
 TTC TTC TTT GAG GCC TAC ATC GGC AAA ATG AGG AAA ACA ACG AAA GCT GAA TAG 1003

 TGTGGAAGCTGAGGAGGAGCCATAGCTCAGGGTCATCAAGAAAAAATAATAGACAAAAGAAAAATGGCACAAGGAATCAC 1082
 ACGTGGTGCAGCTAAAAACAAAACATGAGCAAAACACAAAACCCCAAGGCAGCTTAGGGATAATTAGGTTGATTAA 1161

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Fig. 18B

CCCAGTAAAGTTTATGATCCCTTTTAGGGTGAGGACTCACTGAGTGCACCTCCATCTCCAAGCACTGCTGCTGGAAGACCC 1240
 CATTCCTCTTTATCTATCAACTCTAGGACAAGGAGAACAAAAGCAAGCCAGAGAGAGAGACTAATCAAAGGCAA 1319
 ACAAAGGCTATTAAACACATAGGAAAAATGTATTACTAAGTGTACATTTCTCTAAGATGAAAAGATTTTACTCTAGA 1398
 AACTGTGCGAGCACAACACACACAATCCCTTTCTAACTTTATGGACACTAAACTGAGCCCAATAGAAAAAGACAAAAATGA 1477
 AAGAGACACAGGGTGTATATCTAGAACGATAATGCTTTTGCAGAAACTAAAGCCCTTTTAAAGAAATGCCAGCTGCTGTA 1556
 GACCCCATGAGAAAAAGATGTTTAAATCATCCTTATGAAAAACAGATGTAAACAACATAATTTCAACTAATCTCATCTTCA 1635
 CTGCATAGCCTCAGGCTAGTGAGTTTGCCAAAAACCAAGGGGTGAATACTTCCCCAAGATTTCTCTGGAGGATGGA 1714
 AACAGTGCAGCCAGGTCCCATGGGGCAGCTCCATCCAGAGCATTTCTGATAGTTGAACTGTAAATTTCTACTCTTAA 1793
 GTGAGATATGAAGCATTATCCTTTTGTTCAGTTGCCCGGCTTTTGAACAGAAAGAGTAAATACAGAAATGAAAAAGAT 1872
 AAACACTCAACCAACAATGTGAAAAACGGGTTCTGTAGTATTTGTAAAAAGGCCCGCCAGGACCACCTGTGAGCTGGA 1951
 AAAGGGAGAAAGCAGTGGGAAAAGAGGTGAGCCGAAGATCAATTCGACAGACAGACGGTGTGTATGCCCTCCCTGTT 2030
 TGACTTCACACACACTCATAACTTTCAAATGAAACCCACAGTATAGCGCATATTTTCGATATTTTGTGAAATTCCAA 2109
 AAGGAAATCACAGGGCTGTTTCGAAATATTTGGGGAAACACTGTGTTTCTGCATCATCTGCATTTGCTCCCCAAGCAATGT 2188
 AGAGGTGTTTAAAGGGCCCTCTGCTGGCTGAGTGGCAATCTACAAACAACCTTCAAGGCAAGTTTGGCTGAAAAACAGTT 2267
 GACAAACAAGGGCCCCATACACTTATCCCTCAAATTTAAAGTGATATGAAATACTTGTCACTGCTTTGGCCAAATCAG 2346
 AAGATATTCACTCCTGCTTCAAGTCAGCTTCAGAAATGTTTAAAGGGACTTTAGCTCTGGAACCTCAAAATCAATTTAT 2425
 TAAGAGCCATATTCTTTAAAAAAAAGCTGGATAATATCTCTGTAAATATTTCAAGTCCTTTACAAGCCAAATACATG 2504
 TGTCAAATGTTTCTAGTATTTCAAAGAAGCAATATATGTAAGTTGTTCAATGTGACATAATAGTATTATAATTGGTTAAG 2583
 TAGCTTAATGATTAGGCAAACTAGATGAAAAGATTAGGGCTTCCACACTGCATAGATTACACGCACATAGCCACGCAT 2662
 ACACACACAGACACACAGATGTGGGGTACACTGAACTTCAAAGCCCAAAATGAATAGAAAAACACATTTTCTGGCTAGCAGA 2741
 AAAAAACAAAACAAAACTGTGTGTTTCTCTTTCTTGCTTTGAGAGTGTACAGTAAAAAGGGATTTTTCGAATATTTTA 2820
 TATTATTTAGCTTTAAATTGTGCTGTCGTTTCATGAAAACAGAGCTGCTCTGCTTTTCTGTGAGAGATGGCAAGGCTTTT 2899
 TCAGCATCTCGTTTATGTGTGGAAATTTAAAAAGAAATAAAGTTTATTCATTTCTGTGTGAAAAAATAAAAAA 2978
 AAAAAAATAA

Fig. 18C

L	K	Q	S	V	C	D	Q	S	F	Y	N	G	P	V	S	K	F	W	19	
GC	CTG	AAG	CAG	TCA	GTT	TGT	GAC	CAG	AGT	TTT	TAC	AAT	GGA	CCT	GTC	AGC	AAA	TTC	TGG	59
A	Y	A	F	V	L	S	K	A	P	E	L	G	D	T	I	F	I	I	L	39
GCT	TAT	GCA	TTT	GTG	CTC	AGC	AAA	GCA	CCC	GAA	CTA	GGT	GAC	ACG	ATA	TTC	ATC	ATT	CTG	119
R	K	Q	K	L	I	F	L	H	W	Y	H	H	I	T	V	L	L	Y	S	59
AGG	AAA	CAG	AAA	CTG	ATC	TTC	CTG	CAC	TGG	TAC	CAC	CAC	ATC	ACT	GTG	CTC	CTG	TAC	TCC	179
W	Y	S	Y	K	D	M	V	A	G	G	G	W	F	M	T	M	N	Y	G	79
TGG	TAC	TCC	TAC	AAA	GAC	ATG	GTC	GCT	GGG	GGT	GGT	TGG	TTC	ATG	ACT	ATG	AAC	TAT	GGC	239
V	H	A	V	M	Y	S	Y	Y	A	L	R	A	A	G	F	R	V	S	R	99
GTG	CAT	GCC	GTC	ATG	TAC	TCT	TAC	TAC	GCC	TTG	CGG	GCT	GCG	GGT	TTC	CGA	GTC	TCC	CGG	299
K	F	A	M	F	I	T	L	S	Q	I	T	Q	M	L	M	G	C	V	I	119
AAG	TTT	GCC	ATG	TTC	ATC	ACC	TTG	TCC	CAG	ATC	ACT	CAG	ATG	CTG	ATG	GGC	TGT	GTC	ATT	359
N	Y	L	V	F	N	W	M	Q	H	D	N	D	Q	C	Y	S	H	F	Q	139
AAC	TAC	CTG	GTC	TTC	AAC	TGG	ATG	CAG	CAT	GAC	AAC	GAC	CAG	TGC	TAC	TCC	CAC	TTT	CAG	419
N	I	F	W	S	S	L	M	Y	L	S	Y	L	V	L	F	C	H	F	F	159
AAC	ATC	TTC	TGG	TCC	TCG	CTC	ATG	TAC	CTC	AGC	TAC	CTT	GTG	CTC	TTC	TGC	CAT	TTC	TTC	479

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Fig. 18E

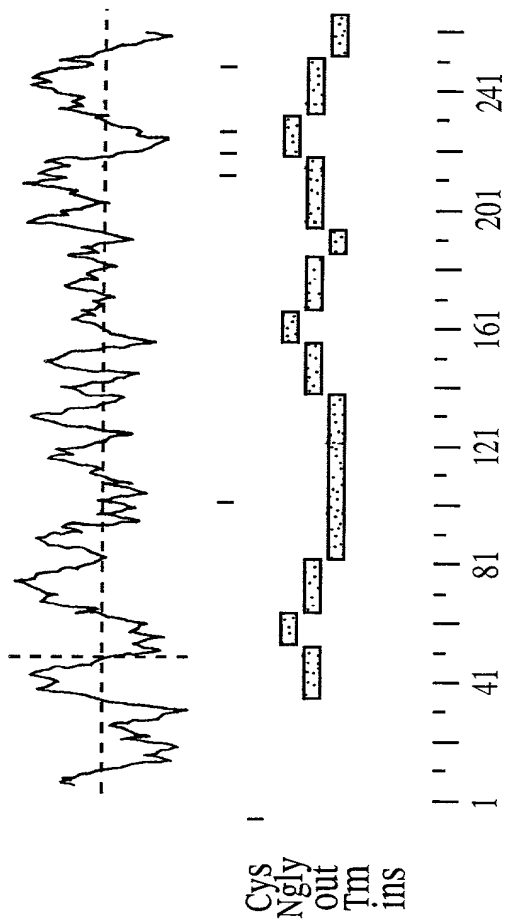


FIG. 18D

F E A Y I G K V K A T K A E *

TTT GAG GCC TAC ATC GGC AAA GTG AAG AAA GCC ACG AAG GCT GAG TAG 175
527

TGTCAGGGCTGAGGAGGAAGTCATAGCTCAGGGTCATCAGGAAAAATATCGACAAAAAATGGCACAAAGGAATCC 606
CATATGGTGCAGCTAAACAAACAAACATCCGTATGAGCAGGCACGAGGCCCAAGGCAGCTTGGGACTGAAGATTAG 685
GTTGTAAGTTTATGATCCCTTCTGGGTGAGGACTCGCTGAGTGCACCTTATCTCAAAGCACGCTGCTGAGGGGACC 764
CCTTCCCTCTGGCCCTGTCAACTCTAGAAACACACTAGATGCAAAAGGCAGCCACGGGCAAGAGATTGGGCAGAGATTAGT 843
GGACGGCCAGCAAAACACTGCAGGAAGCAGGTGGGGGAGGAATCTACTCAGCCCTTTTGTGTTTGTGTTTGTGTTT 922
GTTTCTCTAAGGATAAAGGAGTTTCCCCTTTTCAAACGATGTAGCACACACACACACACACACACACACACA 1001
CACACACACACACGCAATCTTTTCAAACGAAACAGAGCTAAAGAAAGATAAACAATGGAGAGACAGGTTTCTAT 1080
CTGGGACAGCAATGCTTTTGCAAAAGGCTAGGCCCTTTTAAAGAAAGGTGAGCTTGTAATCTCTTGATAAAAGATGCTT 1159
AATTATTTTACTGCAACTGAAAGTAAGAGGTAGAGCCCTTTCCCCTTCTGCACAGCCCTCAGGGCTTGATGTTCTCTA 1238
CAACCAACACACAGGACAGTACTTCCCCTATGATACCTTATTACTGGGAGAAAGAACCCCTGTAGTTGAAACACACAC 1317
TGACAACTGTTATTTCTGCTCTCCGACGAGAAATTCAGCATCCGTTGTTTCAAGTTGCCCCAAACTTTAGGACGGAGGT 1396
AAATGCAGAACTGAAAGGGAAGAGCTCAGCTGGCTGGCTTGAAAAATGGAGTCTTGTAACCATGTGTAACAAATGCCAGC 1475
CCATCGTCCCTGGAGCTGAACAGGGAGGAAGGCTATGGGCAGAGACTAGAGCCGATTCATCCATGTGCAGACAGCG 1554
TGTTCCGCTCCCTCCCTGTTTCGACCTCACACATAATCCTGGCTTCTAAATGAGGCCCTGTGACACACTCTGTGCTTTC 1633
TATATTTTGTGACTTTCAAACACAGATCTGCAGGGCTCTGCCCTGATTTGGGGTAAACACTGTGTTTCTGCAGCCTCTG 1712
CATTTGCTCCCTTCAGCAGTGCAGAGGCTTGAGAAAGTGCCCTCTGCTGGCTTAGTGAGAAGCTTCAACAAACACTTCAC 1791
AGTAGGTTGAAATAACTGACCACTAAGGCCCTGCGGAGATTAAACCCCTAAGTCTAAGTGTCTCAAAACACCTGACATA 1870
TATTTGACCAAAATCAGAAAGAGAGAGAAACCTCTATGCTTCAAGTAAGCGTCAATAAATTTTTTAAGTGACTTTCACCTG 1949
AGAACTCAGAAAGTCAATGTATTAAAGGCCATATTCTGAAAGAAAGAAAGAGAAAGAAAGAAAGAAAAA 2028
AAAA 2032

Fig. 18F

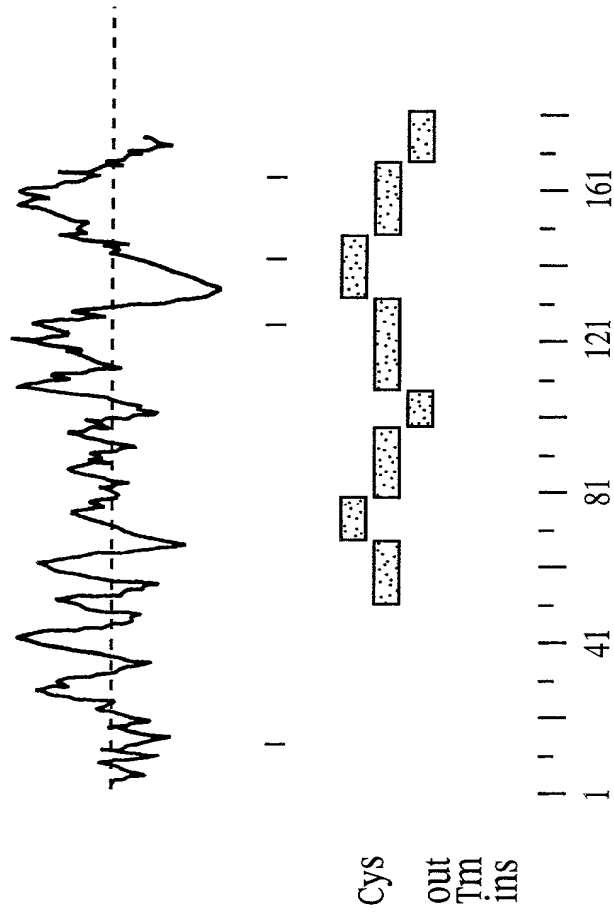


FIG. 186

human	MNMSVLTLLQEYEFKQFNENEAIQWMQENWKKSF	10	20	30	40	50	60	70
murine	-----							
human	AVFSIFGALRTGAYMVYILMTKGLKQSVCDQGFYNGPVS	80	90	100	110	120	130	140
murine	-----							
human	HWYHHITVLLYSWYSYKDMVAGGWFMTMNYGVHVMYSYALRAAGFRVSRKFAMFITLSQITQMLMGC	150	160	170	180	190	200	210
murine	-----							
human	VVNVLVFCWMQHD--QCHSHFQNI	220	230	240	250	260		
murine	-----							

Fig. 18H

human	ATGAACATGTCAGTGTGACTTTACAAGAATATGAATTCGAAAAGCAGTTC AACGAGAATGAAGCCATCC	10	20	30	40	50	60	70
murine	-----							
human	AATGGATGCAGGAAACTGGAAGAAATCTTTCCCTGTTTCTGCTCTGTATGCTGCCCTTTATATTCGGTGG	80	90	100	110	120	130	140
murine	-----							
human	TCGGCACCTAATGAATAAACGAGCAAAGTTTGAACTGAGGAAGCCATTAGTGCTCTGGTCTCTGACCCCTT	150	160	170	180	190	200	210
murine	-----							
human	GCAGTCTTCAGTATATTCCGGTGCTCTTCGAACTGGTGCTTATATGTTGATGACCAAAGGCC	220	230	240	250	260	270	280
murine	-----							

Fig. 18I

human	290	300	310	320	330	340	350
	TGAAGCAGTCAGTTTGTGACCCAGGGTTTTTACAATGGACCTGTCAGCAAATTCCTGGGCTTATGCATTGTG						
	::						
murine	TGAAGCAGTCAGTTTGTGACCCAGAGTTTTTACAATGGACCTGTCAGCAAATTCCTGGGCTTATGCATTGTG						
	10	20	30	40	50	60	70
human	360	370	380	390	400	410	420
	GCTAAGCAAAGCACCCGAACTAGGAGATACAAATATTCATTATCTGAGGAAGCAGAAAGCTGATCTTCCTG						
	::: ::						
murine	GCTCAGCAAAGCACCCGAACTAGGTGACACGATATTCATCATTCTGAGGAAAACAGAAAAGCTGATCTTCCTG						
	80	90	100	110	120	130	140
human	430	440	450	460	470	480	490
	CACTGGTATCACCCACATCACTGTGCTCCTGTACTCTTGGTACTCCTACAAAGACATGGTTCCTGGGGGAG						
	::::::::: :: :: ::::::::::						
murine	CACTGGTACCACCCACATCACTGTGCTCCTGTACTCCTGGTACTCCTACAAAGACATGGTCGTGGGGGTG						
	150	160	170	180	190	200	210
human	500	510	520	530	540	550	560
	GTTGGTTTCATGACTATGAACATATGGCGTGACGCCGTGATGTACTCTTACTATGCCCTTTCGGGGCGGCAGG						
	::						
murine	GTTGGTTTCATGACTATGAACATATGGCGTGACGCCGTGATGTACTCTTACTACGCCCTTTCGGGGCTGCGGG						
	220	230	240	250	260	270	280

Fig. 18J

	570	580	590	600	610	620	630
human	TTTCCGAGTCTCCCGAAGTTTGCCATGTTCA	CACCTTG	TCCAGATCA	CTCAGATG	CTGATGGG	CTGT	
	290	300	310	320	330	340	350
murine	TTTCCGAGTCTCCCGAAGTTTGCCATGTTCA	CACCTTG	TCCAGATCA	CTCAGATG	CTGATGGG	CTGT	
	640	650	660	670	680	690	
human	GTGGTTAACTACCTGGTCTTCTGCTGGATGC	AGCATGAC	-----	CAGTGTCA	CTCTCACTTT	TTCAGAAACA	
	360	370	380	390	400	410	420
murine	GTCATTAACTACCTGGTCTTCAACTGGATGC	AGCATGAC	AAACGACG	AGTGTACT	CTCCACTTT	TTCAGAAACA	
	700	710	720	730	740	750	760
human	TCTTCTGGTCCCTCACTCATGTACCTCAGCT	ACCTTGT	GTCTCTTCTGCC	ATTCTTCT	TGAGGC	CTACAT	
	430	440	450	460	470	480	490
murine	TCTTCTGGTCCCTCACTCATGTACCTCAGCT	ACCTTGT	GTCTCTTCTGCC	ATTCTTCT	TGAGGC	CTACAT	
	770	780	790				
human	CGGCAAAATGAGGAAAACAAACGAAAGCTGAA						
	500	510	520				
murine	CGGCAAAAGTGAAGAAAAGCCACGAAGGCTGAG						

Fig. 18K

GenBank: U04696.60

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10      20      30      40      50      60
I400 ATGAACATGTCAGTGTGTGACTTTACAAGAAATATGAATT--CGAAAGCAGTTCAACGAGAAATGAAGC--
      :::::::::: : :: ::::::::::: : ::::::::::: : : : : : ::::
CIG30 ATGGACACATCCATGAATTTCTCACGCGGGTTAAAAATGGACCTGATGCAACCCCTATGACTTTCGAGACGT
      10      20      30      40      50      60      70

70
I400 --CA--TCCAATGG-----ATGCAGGAAAACTGGAAGAAATCTTTCCCT-GTTTTCTGC-TCTGTATGCT
      :: :: ::::: :: ::::::::::: ::::: : : : : : : ::::: : : :
CIG30 TTCAGGACTTAAGGCCCTTTTGGAGGAGTACTGGGTAAGCTCATTTCTCATAGTGGTCGTCATCTGTT
      80      90      100      110      120      130      140

130      140      150      160      170      180      190
I400 GCCTTTATATTTCGGTGGTTCGGCACCTA-ATGAATAAACGAGCAAAGTTTGAACT-GAGGAAGCCATTAGT
      :: : :: : : ::::: ::::: ::::: ::::: : : : : : : : : : : :
CIG30 GC--TCATCGTTGTTGGCCAG-ACCTACATGAGAACGCCGA-AGAGCTTCAGCTTGCAGAGGCCCTCTCAT
      150      160      170      180      190      200

200      210      220      230      240      250      260
I400 GCTCTGGTCTCTGACCCCTTGCAGTCTTCAGTATATTTCGGTGCCTTCGAACTGGTGCTTATATGGTGTA
      ::::::::::: : . ::::: ::::::::::: : ::::::::::: : : : : : : : :
CIG30 CCTCTGGTCCTTCTTCCTGGCAATATTCAGTATCCTGGGTACTCTGAGGATGTGGAAGTTTATGGCAACA
      210      220      230      240      250      260      270

```

Fig. 18M

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270      280      290      300      310      320
I400 ATTTTGATGACCAAGGCCTGAAGCAGTCAGTTTG--TGACCAGGGTTTTTACAATGGAC-CTGTCAGCA
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
CIG30 GTGATGTTTACAGTGGGCCTCAAGCAAACCGTGTGCTTTTGCCA--TCTACACGGATGACGCCGTAGTCA
    280      290      300      310      320      330      340

330      340      350      360      370      380      390
I400 AATTCTGGCCTTATGCATTTGTGCTAAGCAAAGCACCCGAACTAGGAGATACAATATTCAATTATTCTGAG
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
CIG30 GATTCCTGGTCCCTTTCTCTCTTCTTCTCTCAGCAAAGGTTGTTGAACTGGGAGACACGGCCTTCATCATCCTGCG
    350      360      370      380      390      400      410

400      410      420      430      440      450      460
I400 GAAGCAGAAGCTGATCTTCCCTGCACCTGGTATCACCCACATCACTGTGCTCCTGTACTCTTGGTACTCCTAC
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
CIG30 TAAGCGTCCACTCATCTTTTGTCCACTGGTACCACCCACAGCACAGTGCTACTGTTCACAAGCTTTGGGATAC
    420      430      440      450      460      470      480

470      480      490      500      510      520      530
I400 AAAGACATGGTTGCCCGG-GGGAGGTTGGTTCATGACTATGAACCTATGGCGTGCACGCCGTGATGTACTCT
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
CIG30 AAGAACAAAGT-GCCTTCGGGTGGCTGGTTCATGACCATGAACCTTTGGCGTCCATTCTGTCTATGTACACT
    490      500      510      520      530      540      550

```

Fig. 18N

Figure 180

```

540      550      560      570      580      590      600
I400 TACTATGCCCTTGC GGCGGCAGGTTTCCGAGTCTCCCGAAGTTTGCC--ATGTTCAACCTTGTTCC--
      ::::: :: ::::: :: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
CIG30 TACTACACTATGAAGGCTGCCAAA--CTGAAGCATCCCTAATCTTCTCCCCATGGTCAATCACCCAG--CCTG
      560      570      580      590      600      610

610      620      630      640      650      660      670
I400 CAGATCACT-CAGATGCTGATGGGCTGTGTGTTAACTACCTGGTCTTCTGCTGGATGCAGCATGACCAG
      ::::: :: ::::: :: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
CIG30 CAGAT-TCTGCAGATGGTTCTGCGCACCATCTTTGGCATACTGAATTACATCTGAGGCAGGAGAAAAGGA
      620      630      640      650      660      670      680

680      690      700      710      720      730      740
I400 TGTCACTCTCACTTTCAGAACAA--TCTTCTGGTCCCTCACTCATGTACCTCAGCTACCTTGTGCTCTTCTG
      :: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
CIG30 TGCCACACAA-ACAA-CGGAACACTTCTTCTGCTGTTTATGCTATATGGGACCTATTTTCATCCTATTTCGC
      690      700      710      720      730      740      750

750      760      770      780      790
I400 CCATTCTTCTTTGAGGCCCTACATCGG--CAAAATGAGGAAAACAAC-GAAAGCTGAA
      :: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
CIG30 TCACTTCTTCCACCGAGCCTACCTCAGGCCCAAGGGCAAAGTTGCATCCCAAGAGCC-AA
      760      770      780      790      800      810

```

Fig. 180

L	G	D	T	I	F	I	I	L	R	K	Q	K	L	I	F	L	H	W	Y	20
CTA	GGT	GAT	ACG	ATA	TTC	ATC	ATT	CTG	AGG	AAG	CAG	AAG	CTG	ATC	TTC	CTG	CAC	TGG	TAC	60
H	H	I	T	V	L	L	Y	S	W	Y	S	Y	K	D	M	V	A	G	G	40
CAC	CAC	ATC	ACT	GTG	CTC	CTG	TAC	TCT	TGG	TAC	TCC	TAC	AAA	GAC	ATG	GTA	GCT	GGG	GGT	120
G	W	F	M	T	M	N	Y	G	V	H	A	V	M	Y	S	Y	Y	A	L	60
GGT	TGG	TTC	ATG	ACT	ATG	AAC	TAT	GGC	GTA	CAC	GCC	GTC	ATG	TAC	TCT	TAC	TAC	GCC	TTG	180
R	A	A	G	F	R	V	S	R	K	F	A	M	F	I	T	L	S	Q	I	80
CGG	GCT	GCG	GGT	TTC	CGG	GTC	TCC	CGG	AAG	TTT	GCC	ATG	TTC	ATC	ACG	TTG	TCC	CAG	ATC	240
T	Q	M	L	M	G	C	V	I	N	Y	L	V	F	N	W	M	Q	H	D	100
ACT	CAG	ATG	CTG	ATG	GGC	TGT	GTC	ATT	AAC	TAC	CTG	GTC	TTC	AAC	TGG	ATG	CAG	CAT	GAC	300
N	D	Q	C	Y	S	H	F	Q	N	I	F	W	S	S	L	M	Y	L	S	120
AAT	GAC	CAG	TGC	TAC	TCC	CAC	TTT	CAG	AAC	ATC	TTC	TGG	TCC	TCA	CTC	ATG	TAC	CTC	AGC	360
Y	L	L	L	F	C	H	F	F	F	E	A	Y	I	G	K	V	K	K	A	140
TAC	CTT	CTG	CTC	TTC	TGC	CAT	TTC	TTC	TTT	GAG	GCC	TAC	ATC	GGC	AAA	GTG	AAG	AAA	GCG	420
T	K	A	E	*																145
ACG	AAG	GCC	GAG	TAG																435

Fig. 18P

TGTGAGAGCTGAGGAGGAAGACATAGCTCAGGGTCATCAGGAAAAATAATAGACAAAAAGAAAAATGGCACAAAGGAATCA 514
 CATATGGTGCAGCTAAAAACAAAAACATTTATGAGCAGACGCTAAGCCCAAGGCAGCTTGGGAGTGAAAGATTAGGTT 593
 GTAAGTTTATGATCCCTTTTGGGTGAGGACTCACTGAGAAACACTGCTGCTGAGGGACCCCTTCCCTCTTACCTGTCAA 672
 CTCTAGAAACACACTAGAAAGCCAAAGGCAGCCATGGGCAAGGAGATTAGTGGACAGCAAGCAAAACACTGCAGGAAGAGGG 751
 GGGAGATCTATTTCAGAGTTTCTGTTTCTGTTTCTCTAAGGATAAAGGAGTTTCCCTTTTCAAACTG 830
 TGTGAGCACACCCACGCGCATGCAGACACACCCACCTACACACTATCTGCAGATGACCAAGTGTCCCTATGCTGTTTTCAC 909
 AAATAAACTTGAGACAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 974

Fig. 18Q

Fig. 18R

GTCGACCCACGCGTCCGGGAGCGGGCTAAGAGTCCCGCACCGCCTCACAACCTGGGAACCGGAGAGTAGGGCCGTC	79
GGCTGGCAAGAACCCGCGTGCCCTCCTCGGCAAGGGCCATCCGGTGCCACCCCATGTCCGCACTAGACAGAAGAGGGTGA	158
<div> <div>M</div> <div>T</div> <div>W</div> <div>L</div> <div>V</div> </div>	
GTCCTGAACCTGCACAGAGCTGCTCTGTACTGTCCCTGGTGGTCCCGCC ATG ACC TGG TTG GTG	5 229
L L G T L L C M L R V G L G T P D S E G	25
CTG CTG GGG ACA CTG CTC TGC ATG CTG CGC GTT GGG TTA GGC ACC CCG GAC TCC GAG GGT	289
F P P R A L H N C P Y K C I C A A D L L	45
TTC CCG CCC CGT GCG CTC CAC AAC TGC CCC TAC AAA TGT ATC TGC GCT GCC GAC CTG CTA	349
S C T G L G L Q D V P A E L P A A T A D	65
AGC TGC ACT GGC CTA GGG CTG CAG GAC GTG CCA GCC GAG TTA CCT GCC GCT ACT GCG GAC	409
L D L S H N A L Q R L R P G W L A P L F	85
CTC GAC CTG AGC CAC AAC GCG CTC CAG CGC CTG CGC CCC GGC TGG TTG GCG CCC CTC TTC	469
Q L R A L H L D H N E L D A L G R G V F	105
CAG CTG CGC GCC CTG CAC CTA GAC CAC AAC GAA CTA GAT GCG CTG GGT CGC GGC GTC TTC	529
V N A S G L R L L D L S S N T L R A L G	125
GTC AAC GCC AGC GGC CTG AGG CTG CTC GAT CTA TCA TCT AAC ACG TTG CGG GCG CTT GGC	589

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Fig. 19A

R	H	D	L	D	G	L	G	A	L	E	K	L	L	L	F	N	N	R	L	145
CGC	CAC	GAC	CTC	GAC	GGG	CTG	GGG	GCG	CTG	GAG	AAG	CTG	CTT	CTG	TTC	AAT	AAC	CGC	TTG	649
V	H	L	D	E	H	A	F	H	G	L	R	A	L	S	H	L	Y	L	G	165
GTG	CAC	TTG	GAC	GAG	CAT	GCC	TTC	CAC	GGC	CTG	CGC	CTC	AGC	AGC	CAT	CTC	TAC	CTG	GGC	709
C	N	E	L	A	S	F	S	F	D	H	L	H	G	L	S	A	T	H	L	185
TGC	AAC	GAA	CTC	GCC	TCG	TTC	TCC	TTC	GAC	CAC	CTG	CAC	GGT	CTG	AGC	GCC	ACC	CAC	CTG	769
L	T	L	D	L	S	S	N	R	L	G	H	I	S	V	P	E	L	A	A	205
CTT	ACT	CTG	GAC	CTC	TCC	TCC	AAC	CGG	CTG	GGA	CAC	ATC	TCC	GTA	CCT	GAG	CTG	GCC	GCG	829
L	P	A	F	L	K	N	G	L	Y	L	H	N	N	P	L	P	C	D	C	225
CTG	CCG	GCC	TTC	CTC	AAG	AAC	GGC	CTC	TAC	TTG	CAC	AAC	AAC	CCT	TTG	CCT	TGC	GAC	TGC	889
R	L	Y	H	L	L	Q	R	W	H	Q	R	G	L	S	A	V	R	D	F	245
CGC	CTC	TAC	CAC	CTG	CTA	CAG	CGC	TGG	CAC	CAG	CGG	GGC	CTG	AGC	GCC	GTG	CGC	GAC	TTT	949
A	R	E	Y	V	C	L	A	F	K	V	P	A	S	R	V	R	F	F	Q	265
GCG	CGC	GAG	TAC	GTA	TGC	TTG	GCC	TTC	AAG	GTA	CCC	GCG	TCC	CGC	GTG	CGC	TTC	TTC	CAG	1009
H	S	R	V	F	E	N	C	S	S	A	P	A	L	G	L	K	R	P	E	285
CAC	AGC	CGC	GTC	TTT	GAG	AAC	TGC	TCG	TCG	GCC	CCA	GCT	CTT	GGC	CTA	AAG	CGG	CCG	GAA	1069

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Fig. 19B

E	H	L	Y	A	L	V	G	R	S	L	R	L	Y	C	N	T	S	V	P	305
GAG	CAC	CTG	TAC	GCG	CTG	GTG	GGT	CGG	TCC	CTG	AGG	CTT	TAC	TGC	AAC	ACC	AGC	GTC	CCG	1129
A	M	R	I	A	W	V	S	P	Q	Q	E	L	L	R	A	P	G	S	R	325
GCC	ATG	CGC	ATT	GCC	TGG	GTT	TCG	CCG	CAG	CAG	GAG	CTT	CTC	AGG	GCG	CCA	GGA	TCC	CGC	1189
D	G	S	I	A	V	L	A	D	G	S	L	A	I	G	N	V	Q	E	Q	345
GAT	GGC	AGC	ATC	GCG	GTG	CTG	GCC	GAC	GGC	AGC	TTG	GCC	ATA	GGC	AAC	GTA	CAG	GAG	CAG	1249
H	A	G	L	F	V	C	L	A	T	G	P	R	L	H	H	N	Q	T	H	365
CAT	GCG	GGA	CTC	TTC	GTG	TGC	CTG	GCC	ACT	GGG	CCC	CGC	CTG	CAC	CAC	AAC	CAG	ACG	CAC	1309
E	Y	N	V	S	V	H	F	P	R	P	E	P	E	A	F	N	T	G	F	385
GAG	TAC	AAC	GTG	AGC	GTG	CAC	TTT	CCG	CGC	CCA	GAG	CCC	GAG	GCT	TTC	AAC	ACA	GGC	TTC	1369
T	T	L	L	G	C	A	V	G	L	V	L	V	L	L	Y	L	F	A	P	405
ACC	ACA	CTG	CTG	GGC	TGT	GCC	GTG	GGC	CTT	GTG	CTC	GTG	CTG	CTC	TAC	CTG	TTC	GCC	CCA	1429
P	C	R	C	C	R	R	A	C	P	L	P	P	L	A	P	N	T	Q	P	425
CCC	TGC	CGC	TGC	TGC	CGC	CGT	GCC	TGC	CCG	CTG	CCG	CCG	CTG	GCC	CCA	AAC	ACC	CAG	CCC	1489
A	P	R	A	E	P	H	K	S	S	V	L	S	T	T	P	P	D	A	P	445
GCT	CCA	AGA	GCT	GAG	CCG	CAC	AAG	TCC	TCA	GTA	CTC	AGC	ACC	ACA	CCG	CCA	GAC	GCA	CCC	1549

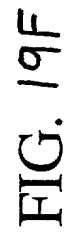
Fig. 19C

S	P	Q	G	A	S	T	S	T	*	
AGC	CCG	CAA	GGC	CAA	GCG	TCC	ACA	AGC	ACG	TAG
TCTTTCTGGAGCCAGGCCGAGGGCCCTCAATGGCCCCGCGTGCACTGGCAGCTGGCAGTAGCTGAGGAATTGATCTCTACAACC	1661									
CTGAGGCCCTGCAGCTGAAGGCTGGCTCTGAGTCCGCCAGCTCCATAGGCTCCGAGGGTCCCATGACAACCTAGACTGC	1740									
CAGGGCTCCCCACCCAGGCCCCCAACCCTCTTGCTGCTCGCCCTGCTCCCTGCTTCGGTCCAGAGAACTGGCAGATACT	1819									
GGTGGGAAGCACTGTGCCTGGCCCCCCCCAGCTTCCTGTATGGGCCCTCGAAACACAAATGGGCCCTTCTCGCTCACTGGTAGA	1898									
GACAGGGGTTGTGTTCCCCCAACCTGCCCCTTCTGCTCTGCCCCCTGCACAGGACCCAAAGGCCCCAGGCCCTGCAAAGGTGTG	1977									
CTAGTTCCCTGCTTTCCCCGGGACTTCCTAGTGCCCCAAATGCCCTGTGAGGCTGAGAGACCCAGGCCCTGTGGCTTTCA	2056									
ACACAGCACAGCTGTGGAAGTGGCTGTGTTCTTCTACAGCCTGTGGAAGAACCCCTGTAGCAGAGCCTCCCCATCCACCC	2135									
TCAGGGGCTGAGGCAGCTCTCAGGAGTGGTGCTCAAGAGCTGACGCGAGGCCACCTCCCCCTTCCCAAGGGGTGGGAG	2214									
GGAGTGGGCCACAGGGAAGAAAGGCGGCTCTGAAGGAAGATCTCGCCCCACACCCAGGACAGAAAGAGGAACAAGC	2293									
CCGCCCTCTGGTGAAATGGGACTCCCTCCATCCACCAACACCCAAACCTCCTGAAAAGCTTCACAACCTTCCGCAGAGTCC	2372									
GGTGGCAGGCACCGCAGGAAAGGCTCCTCAAGAGGTTCCCTGGTGTCTGGCCTAAGCCCCAGCCAGAGGCCCTGCTC	2451									

Fig. 19D

TCTCTGGCCTGGGGCATCCACCCGTTGTTCTGAAGCAGAGCCCATTTCTGTGGGCTCACAAGACACAGTGAAGGGGATC 2530
 ATGGCCCTGCACCCCTGCTTTTCAGCAGTAAAAAGCCCGAAAGCCTGGCGAGCATGGCCGAGCTGGGAGGCCGAGCCG 2609
 GAACTCCACGTCCTCGAGAGCAGGAGCCCTCTTAAGGGCTGGCACTGGTCTCAGCCCTAATGGCTGAGGCGGTACCCCTGG 2688
 CTTCATATGCATCTCACTGCTCCCACCTGCAGGGGGCAGGGAAGGGGGTCTGGGAGCCCTTCATGTGTGGGGCCGAG 2767
 CTGGGGGCCCCCATGGCCATCCCTGGACCTCGCTGCTCCAGAGTTTAAATAAAGGTAGCACATGCTTATTGCTAGAAAAAA 2846
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 2895

Fig. 19E



	10	20	30	40	50	60	70
H	MTWLVLLGTL	MLRVGLGTPD	SEGFPPRALH	NCYPKICAAD	LLSCTGLGLQD	VPAELPAATAD	LDLSH
	: :	: :	: :	: :	: :	: :	: :
P	MN-LDIHCEQ	LSDARWTELL	PLLQQYEVVR	LLDDCGLTEH	CKDIGS--AL	RANPSLTELCL	RRTNEL--GD
	10	20	30	40	50	60	
	80	90	100	110	120	130	
H	NALQRLRPGW	LAPLFQLRAL	HLDHNELDAL	GRGVFVNA---	SGLRLDLLSS	NTRLALGRHDL	-DGLGA-
	: :	: :	: :	: :	: :	: :
P	AGVHLVLQGL	QSPTCKIQKLS	QNCSLTEAGC	GVLPSTLRS	PTLRELHLS	DNPLGDAGLRL	CEGLDP
	70	80	90	100	110	120	130
	140	150	160	170	180	190	200
H	---LEKLLLF	NNRLVHLD-E	HAFHGLRAL	SHLYLGCNEL	ASFDFDHLH	GLSATHLLTL	DLSSNRLGHISV
	::::	: :	: :	: :	: :	: :	: :
P	QCHLEKLQLE	YCRLTAA	SCEPLASVLR	ATRAL----	KELTVSNND--	IGEAGARVLG	QGGLAD-----SA
	140	150	160	170	180	190	
	210	220	230	240	250	260	
H	PELAALPAFL	KN-GLYLHNN	PLPCDCRLYH	LLQRWHQRL	SAVRDFAREY	VCLAFKVPAS	RVR---FFQH
	.:::	: :	: :	: :	: :	: :	: :
P	CQLETLR--	LENCGLTPAN	CKDLCGIVAS	QASLRELDL	GSNGLGDA	GIAELCPGLL	SPASRLKTLWLWEC
	200	210	220	230	240	250	260

Fig. 19G

```

270      280      290      300      310      320
H SRVFENCSSA-PALGLKRPEEHLIALVGRSL-----RLYCNTSV-PAMRIAWVSPQQELLRAPGSRDGS
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
P DITASGCRDLCRVLAQKETLKEI-SLAGNKLGDGARGLLCESLLQPGCQLESILWVKSCSLTAACQHVSL
270      280      290      300      310      320      330

330      340      350      360      370      380      390
H AVLADGSLAIGNVQEQHAGLFVCLATGPRLHHNQTHEYNVSVHFFRPEPEAFNTGFTLLGCAVGLVLVL
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
P MLTQNKHL-----LEIQSSNKLGDSDGIQELCQALSQPGTTLRVLCIGDCEVTNSGCSSLAS--LLANRS
340      350      360      370      380      390

400      410      420      430      440      450
H LYLFAPPCRRACPLPPLAPNTQPAPRAEPHK-SSVLSTTPPDAPSPQQASTS-----T
: . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
P LRELDLSNNCVGDPGVQLQLGSLEQPGCALEQLVLYDTYWTEEVEDRLQALEGSKPGLRVIS
400      410      420      430      440      450

```

Fig. 19H

Sequence

ccg ttt ctc ttt aac cac ttg cac ggt ctg ggg tta acc cgc ctg cgg	48
Pro Phe Leu Phe Asn His Leu His Gly Leu Thr Arg Leu Arg	
1 5 10 15	
act ctg gac ctc tcc tcc aac tgg ctg aaa cat atc tcc atc cct gag	96
Thr Leu Asp Leu Ser Ser Ser Asn Trp Leu Lys His Ile Ser Ile Pro Glu	
20 25 30	
ttg gct gca ctg cca act tat ctc aag aac agg ctc tac ctg cac aac	144
Leu Ala Ala Leu Pro Thr Tyr Leu Lys Asn Arg Leu Tyr Leu His Asn	
35 40 45	
aac ccg ctg ccc tgt gac tgc agc ctc tac cac ctg ctc cgg cgc tgg	192
Asn Pro Leu Pro Cys Asp Cys Ser Leu Tyr His Leu Leu Arg Arg Trp	
50 55 60	
cac cag cgg ggc ctg agt gcc ctg cat gat ttt gaa cgc gag tac aca	240
His Gln Arg Gly Leu Ser Ser Ala Leu His Asp Phe Glu Arg Glu Tyr Thr	
65 70 75 80	
tgc ttg gtc ttt aag gtg tca gag tcc cga gtg cgc ttt ttt gag cac	288
Cys Leu Val Phe Lys Val Ser Ser Glu Ser Arg Val Arg Phe Phe Glu His	
85 90 95	
agc cgg gtc ttc aag aac tgc tct gtg gct gca gct cca ggc tta gag	336
Ser Arg Val Phe Lys Asn Cys Ser Val Ala Ala Ala Pro Gly Leu Glu	
100 105 110	

Fig. 19I

“LIFE”

ctg cct gaa gag cag ctg cac gcg cag gtg ggc cag tcc ctg agg ctc Leu Pro Glu Glu Gln Leu His Ala Gln Val Gly Gln Ser Leu Arg Leu	115 120 125	384
ttc tgc aac acc agt gtg cct gcc act cgg gtg gcc tgg gtc tcc ccg Phe Cys Asn Thr Ser Val Pro Ala Thr Arg Val Ala Trp Val Ser Pro	130 135 140	432
aag aat gag ctg ctt gtg gcg cca gcc tct cag gat ggt agc atc gct Lys Asn Glu Leu Leu Val Ala Pro Ala Ser Gln Asp Gly Ser Ile Ala	145 150 155 160	480
gtg ttg gct gat ggc agc tta gcc ata ggc agg gtg caa gag cag cac Val Leu Ala Asp Gly Ser Leu Ala Ile Gly Arg Val Gln Glu Gln His	165 170 175	528
gca ggc gtc ttt gtg tgc ctg gcc agt ggg ccc cgc ctg cac cac aac Ala Gly Val Phe Val Cys Leu Ala Ser Gly Pro Arg Leu His His Asn	180 185 190	576
cag aca ctt gag tac aat gtg agt gtg caa aag gct cgc ccc gag cca Gln Thr Leu Glu Tyr Asn Val Ser Val Gln Lys Ala Arg Pro Glu Pro	195 200 205	624
gag act ttc aac aca ggc ttt acc acc ctg ggc tgt att gtg ggc Glu Thr Phe Asn Thr Gly Phe Thr Thr Leu Leu Gly Cys Ile Val Gly	210 215 220	672

Fig. 19J

ctg gtg ctg gtg ttg ctc tac ttg ttt gca cca ccc tgt cgt ggc tgc	720
Leu Val Leu Leu Leu Tyr Leu Phe Ala Pro Pro Cys Arg Gly Cys	
225 230 235	
tgt cac tgc tgt cag cgg gcc tgc tgc tgg ccc cgg gca	768
Cys His Cys Cys Gln Arg Ala Cys Arg Asn Arg Cys Trp Pro Arg Ala	
245 250 255	
tcc agt cca ctc cag gag ctg agc gca cag tcc tcc atg ctt agc act	816
Ser Ser Pro Leu Gln Glu Leu Ser Ala Gln Ser Ser Met Leu Ser Thr	
260 265 270	
acg cca cca gat gca ccc agc cgc aag gcc agt gtc cac aag cat gtg	864
Thr Pro Pro Asp Ala Pro Ser Arg Lys Ala Ser Val His Lys His Val	
275 280 285	
gtc ttc ctg gag ccg ggc aag aag ggc ctc aat ggc cgt gtg cag ctc	912
Val Phe Leu Glu Pro Gly Lys Lys Gly Leu Asn Gly Arg Val Gln Leu	
290 295 300	
gca gta cct cca gac tcc gat ctg tgc aac ccc atg ggc ttg caa ctc	960
Ala Val Pro Pro Asp Ser Asp Leu Cys Asn Pro Met Gly Leu Gln Ieu	
305 310 315 320	
aa	962

Fig. 19K

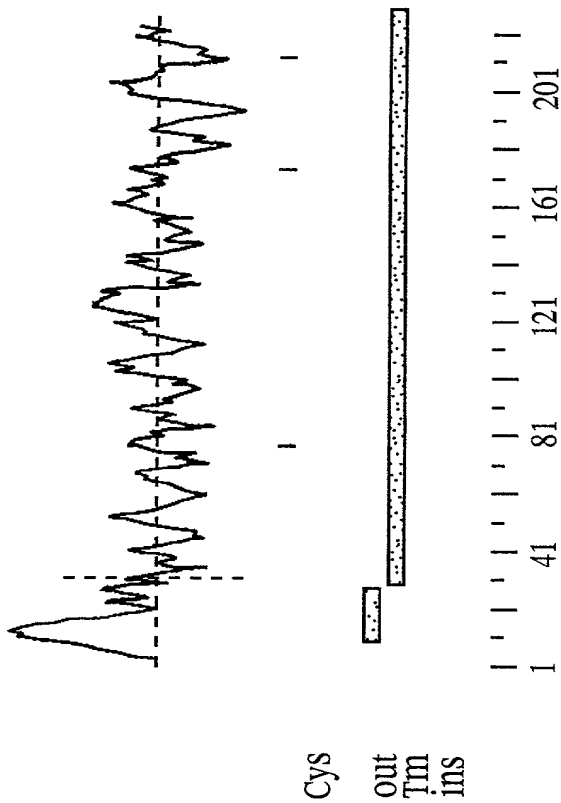


FIG. 19L

“0000” 000000

```

M      1  ..... PFLFNHLHGLTRLRTLDLSSNWLKHISI 30
H    151  HAFHGLRALSHLYLGCNELASFDFDHLHGLSATHLLTLDLSSNRLGHISV 200

M      31  PELAAALPTYLKNRLYLHNNPLPCDCSLYHLLRRWHQRGLSALHDFEREY 80
H    201  PELAAALPAFLKNGLYLHNNPLPCDCRLYHLLQRWHQRGLSAVRDFAREYV 250

M      81  CLVEKVSERVRFFEHRSRVFKNCVAAAPGLELPEEQHQAQVGSRLRFC 130
H    251  CLAFKVPASRVRFQHSRVFENCSSAPALGLKRPEEHLYALVGRSLRYC 300

M     131  NTSVPATRVAVSPKNELLVAPASQDGSIAVLADGSLAIGRVQEQHAGVF 180
H    301  NTSVPAMRIAWVSPQQLLRAPGSRDGSIAVLADGSLAIGNVQEQHAGLF 350

M     181  VCLASGPRLHHNQTFLEYNSVQKARPEPETFNTGTTLLGCIVGLVLVLL 230
H    351  VCLATGPRLHHNQTHEYNVSVHFPRPEAFNTGTTLLGCAVGLVLVLL 400

M     231  YLFAPPCRGCHCCQACRNRNCWPRASSPLQELSA.QSSMLSTTPPDAPS 279
H    401  YLFAPPCR....CCRRACPLPPLAPNTQPAPRAEPHKSSVLSTTPPDAPS 446

M     280  RKASVHKHVVFLEPGKKGLNGRVQLAVPPDSDLCPNPMGLQL 320
H    447  PQGQASTST..... 455

```

Fig. 19M

[illegible]

Fig. 20A

207/361																				
T	I	A	G	L	V	V	G	L	A	D	L	L	S	K	H	D	S	Q	170	
ACC	ATC	GCG	GGG	CTG	GTG	GTC	GTG	GGC	CTG	GCT	GAC	CTC	CTG	AGC	AAG	CAC	GAC	AGT	CAG	549
H	K	L	S	E	V	I	T	G	D	L	L	I	I	M	A	Q	I	I	V	190
CAC	AAG	CTC	AGC	GAA	GTG	ATC	ACA	GGG	GAC	CTG	TTG	ATC	ATC	ATG	GCC	CAG	ATC	ATC	GTT	609
A	I	Q	M	V	L	E	E	K	F	V	Y	K	H	N	V	H	P	L	R	210
GCC	ATC	CAG	ATG	GTG	CTA	GAG	GAG	AAG	TTC	GTC	TAC	AAA	CAC	AAT	GTG	CAC	CCA	CTG	CGG	669
A	V	G	T	E	G	L	F	G	F	V	I	L	S	L	L	L	V	P	M	230
GCA	GTT	GGC	ACT	GAG	GGC	CTC	TTT	GGC	TTT	GTG	ATC	CTC	TCC	CTG	CTG	CTG	GTG	CCC	ATG	729
Y	Y	I	P	A	G	S	F	S	G	N	P	R	G	T	L	E	D	A	L	250
TAC	TAC	ATC	CCC	GCC	GGC	TCC	TTC	AGC	GGA	AAC	CCT	CGT	GGG	ACA	CTG	GAG	GAT	GCA	TTG	789
D	A	F	C	Q	V	G	Q	Q	P	L	I	A	V	A	L	L	G	N	I	270
GAC	GCC	TTC	TGC	CAG	GTG	GGC	CAG	CAG	CCG	CTC	ATT	GCC	GTG	GCA	CTG	CTG	GGC	AAC	ATC	849
S	S	I	A	F	F	N	F	A	G	I	S	V	T	K	E	L	S	A	T	290
AGC	AGC	ATT	GCC	TTC	TTC	AAC	TTC	GCA	GGC	ATC	AGC	GTC	ACC	AAG	GAA	CTG	AGC	GCC	ACC	909
T	R	M	V	L	D	S	L	R	T	V	V	I	W	A	L	S	L	A	L	310
ACC	CGC	ATG	GTG	TTG	GAC	AGC	TTG	CGC	ACC	GTT	GTC	ATC	TGG	GCA	CTG	AGC	CTG	GCA	CTG	969

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Fig. 20B

G W E A F H A L Q L A L L I L G F L I L L I G T 330
 GGC TGG GAG GCC TTC CAT GCA CTG CAG ATC CTT GGC TTC CTC ATA CTC CTT ATA GGC ACT 1029

 A L Y N G L H R P L L L L G R L S R G R P L 350
 GCC CTC TAC AAT GGG CTA CAC CGT CCG CTG CTG GGC CGC CTG TCC AGG GGC CGG CCC CTG 1089

 A E E S E Q E R L L L G G T R T P I N D A 370
 GCA GAG GAG AGC GAG CAG GAG AGA CTG CTG GGT GGC ACC CGC ACT CCC ATC AAT GAT GCC 1149

 S * 372
 AGC TGA 1155

 GGTCCCTGGAGGCTTCTACTGCCACCCGGGTGCTCCTTCTCCCTGAGACTGAGGCCACACAGGCTGGTGGGCCCCGAA 1234
 TGCCCTATCCCCAAGGCCTCACCCCTGTCCCTCCCTGCAGAACCCCAAGGCAGCTGCTGCCACAGAAGATAACAACAC 1313
 CCAAGTCCCTCTTTTCTCACTACCACCTGCAGGGTGGTGTACCCAGCCCCCACAAAGCCTGAGTGCAGTGGCAGACCTC 1392
 AGCTCTCTGGACCCCTCCTACAGCACTAGAGCTAAATCATGAAGTTGAATTGTAGGAATTTACCACCGTAGTGTATCTG 1471
 AATCATAAACTAGATTATCATATAAAAAAAAAAAAAAAAAAGGGCGGCCGC 1518

Fig. 20C

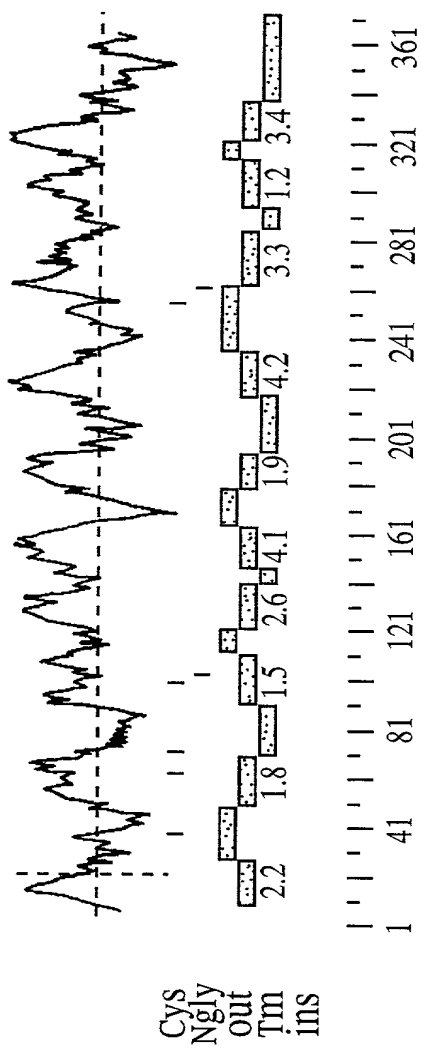


FIG. 20D

GTCGACCCACGCGTCCGGGACAGCTGGCCTGAAGCTCAGAGCCGGGGCGTGCGCC																	M	A	P	H	W	5
ATG GCC CCA CAC TGG																						72
A	V	W	L	L	A	A	R	L	W	G	L	G	I	G	A	E	V	W	W	25		
GCT	GTC	TGG	CTG	CTG	GCA	GCA	AGG	CTG	TGG	GGC	CTG	GGC	ATT	GGG	GCT	GAG	GTG	TGG	TGG	132		
N	L	V	P	R	K	T	V	S	S	G	E	L	A	T	V	V	R	R	F	45		
AAC	CTT	GTG	CCG	CGT	AAG	ACA	GTG	TCT	TCT	GGG	GAG	CTG	GCC	ACG	GTA	GTA	CGG	CGG	TTC	192		
S	Q	T	G	I	Q	D	F	L	T	L	T	L	T	E	P	T	G	L	L	65		
TCC	CAG	ACC	GGC	ATC	CAG	GAC	TTC	CTG	ACA	CTG	ACG	CTG	ACG	GAG	CCC	ACT	GGG	CTT	CTG	252		
Y	V	G	A	R	E	A	L	F	A	F	S	M	E	A	L	E	L	Q	G	85		
TAC	GTG	GGC	GCC	CGA	GAG	GCC	CTG	TTT	GCC	TTC	AGC	ATG	GAG	GCC	CTG	GAG	CTG	CAA	GGA	312		
A	I	S	W	E	A	P	V	E	K	K	T	E	C	I	Q	K	G	K	N	105		
GCG	ATC	TCC	TGG	GAG	GCC	CCC	GTG	GAG	AAG	AAG	ACT	GAG	TGT	ATC	CAG	AAA	GGG	AAG	AAC	372		
N	Q	T	E	C	F	N	F	I	R	F	L	Q	P	Y	N	A	S	H	L	125		
AAC	CAG	ACC	GAG	TGC	TTC	AAC	TTC	ATC	CGC	TTC	CTG	CAG	CCC	TAC	AAT	GCC	TCC	CAC	CTG	432		
Y	V	C	G	T	Y	A	F	Q	P	K	C	T	Y	V	V	S	A	A	L	145		
TAC	GTC	TGT	GGC	ACC	TAC	GCC	TTC	CAG	CCC	AAG	TGC	ACC	TAC	GTC	GTG	AGT	GCT	GCC	CTC	492		

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Fig. 21A

L	P	R	C	P	Q	P	P	A	L	L	T	L	L	W	T	R	G	C	G	165
CTA	CCT	CGG	TGT	CCC	CAG	CCC	CCC	GCC	CTC	CTC	ACC	CTT	CTC	TGG	ACT	CGT	GGA	TGT	GGC	552
P	Q	S	P	A	L	K	H	L	L	I	T	S	L	S	V	L	R	T	C	185
CCA	CAG	AGC	CCT	GCC	CTT	AAG	CAT	CTC	ATC	ACC	TCT	CTC	TCT	TCT	GTC	CTT	AGA	ACA	TGC	612
S	P	S	L	W	S	M	E	S	L	K	M	G	R	A	S	V	P	M	T	205
TCA	CCT	TCA	CTT	TGG	AGC	ATG	GAG	AGT	TTG	AAG	ATG	GGA	AGG	GCA	AGT	GTC	CCT	ATG	ACC	672
Q	L	R	A	M	L	A	F	L	W	M	V	S	C	T	R	P	H	S	T	225
CAG	CTA	AGG	GCC	ATG	CTG	GCC	TTC	TTG	TGG	ATG	GTG	AGC	TGT	ACT	CGG	CCA	CAC	TCA	ACA	732
T	S	W	A	R	N	P	L	S	C	V	T	W	G	P	T	T	P	*		244
ACT	TCC	TGG	GCA	CGG	AAC	CCA	TTA	TCC	TGC	GTA	ACA	TGG	GGC	CCC	ACC	ACT	CCA	TGA		789
AGACAGAGTACCTGGCCCTTTTGGCTCAACGAACCTCACTTTGTAGGCTCTGCCTATGTACCTGAGAGTGTGGCAGCTT																				868
CACGGGGACGACGACAGGTCTACTTCTTTCAGGGAGCGGGCAGTGAGTCCGACTGCTATGCCGAGCAGGTGGTG																				947
GCTCGTGGCCCGTGTCTGCAAGGGCGATATGGGGGGCGCACGGACCCCTGCAGAGGAAGTGGAACACCGTTCTCTGAAGG																				1026
CGCGGCTGGCATGCTCTGCCCCGAACTGGCAGCTCTACTTCAACCAGCTGCAGCGGATGCACACCCCTGCAGGACACCTC																				1105

Fig. 21B

Fig. 21C

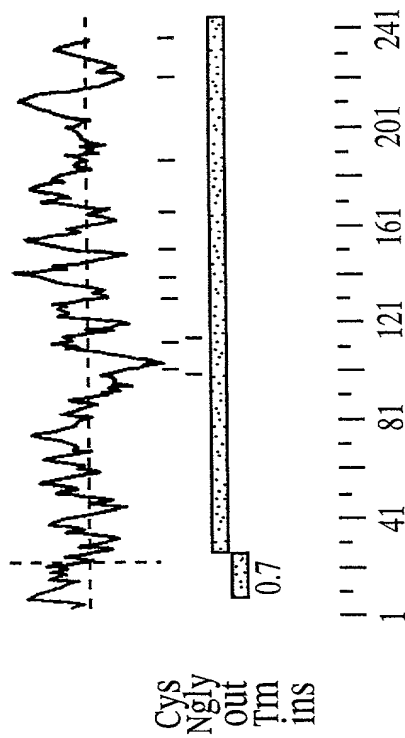


FIG. 2/E

150

Fig. 21F

Cellulose

```

710      720      730      740      750      760      770
M ASERTLVYPLELPKEPASPPFRPGPETDEKLWDPVGYYSYSDGSLKIVPGHARCQPGGGPPSPPPGIPGQP
H -----:-----:-----:-----:-----GPTTP-----
                                     240

780      790      800      810      820      830
M LPSPTRLHLGGGRNSNANGYVRLQLGGEDRGSGHPLPELADELRRKLQQRQLPDSNPPESSV
H -----

```

Fig. 21H

```

360      370      380      390      400      410      420
M QAQKWARYTDPVSPRPGSCINNWHRDNGYTSSLELPDNTLNFIKKHPLMEDQVKPRLGRPLLVKKNNTNF
  ::      ::      ::      ::      ::      ::      ::
H ----WTR-----GCGPQ-----SPAL-----KH-----LLI---TSL
160
430      440      450      460      470      480      490
M THVVADRVPGLDGATYTVLFIGTGDWLLKAVSLGPWIHMVEELQVFDQEPVESLVLSQSKKVLFAGSRS
  .      .      .      .      .      .      .
H S-----VLRTCSPSLW-----SMESLKMGR-----SVPMT
180
500      510      520      530      540      550      560
M QLVQLSLADCTKYRFCVDCVLARDPYCAWNVNTSRCVATTSGRSGSFLVQHVANLDTSKMCNQYGIKKVR
  ::      ::      :      :      :      :      :
H QLRAM-LA-----F-----L-----WMVSCTRPHSTTS-----
210
570      580      590      600      610      620      630
M SIPKNITVVSGETDLVLPCHLSSNLAAHAWTFGSQDLPAEQPGSFLYDTGLQALVVMAAQSRHSGPYRCYS
  :
H -----W-----
640      650      660      670      680      690      700
M EEQGTRLAAESYLVAVVAGSSVTLEARAPLENGLVWLAVVALGAVCLVLLLVLSLRRRLREELEKGA
  ::      ::      ::      ::      ::      ::      ::
H -----ARNPLS-----CVT-----
230

```

Fig. 21G

	290	300	310	320	330	340	350
M	ATTCTGGCCTTTATATGTGGGGCCCGAGAGCGCTGTTTGCCTTCAGTGTAGAGGCTCTGGAGCTGCA						

H	CCACTGGGCTTCTGTACGTGGCGCCCGAGAGGCCCTGTTTGCCTTCAGCATGGAGGCCCTGGAGCTGCA						

Fig. 21I

Fig. 21J

Fig. 21J

Sequence

```

710      720      730      740      750      760      770
M TCAAGACAGATACCTGGCTTTTGGCTGAATGAACCCCACTTTGTAGGCTCTGCCCTTTGTCCCTGAGAG
  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H -----AGAGCCCTGCCCTTAAGC-----ATCTCCTCATCAC---CTCTCTCTGTCC--TTAGA-
560      570      580      590      600

780      790      800      810      820      830      840
M TGTGGGAAGCTTACGGGAGACGATGACAAGATCTACTTCTTTCAGTGAGCGGCAGTGAGATGAC
  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H -----ACATGCTCACCTTCA-CTT-TG-GAGCA---TGGAGAGTTTGA-
610      620      630      640

850      860      870      880      890      900      910
M TGCTATTCCGAGCAGGTGGTGGCTCGTGTGGCGAGAGTCTGTAAAGGTGACATGGGGGAGCAGCAGCGC
  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H -----AGATGG-----GAAGGGCAAGTGTG-----C-----CTATGACCC
650      660      670

920      930      940      950      960      970      980
M TGCAGAAGAAATGGACGACGTTCCCTGAAGGCTCGGTTGGTGTGCTCAGCCCCCTGACTGGAAGTCTACTT
  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H AGCTAAGGGCCATGCTGGCCCTTCTTGT-GGATGTTGAGCTGTACTCGGCCAC--ACT-----CAACAA
680      690      700      710      720      730

990      1000     1010     1020     1030     1040     1050
M CAACCAGCTGAAGGCGGTGCACACCCCTGCGGGGCGCCCTCTTGGCACAAACACCACTTCTTCGGGGTTTTT
  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H CTTCCCTG-----GGCA-----CGGAAC-CCA-TTATC-----CTGCG-----TAA
740      750      760

```

Fig. 21K


```

1060      1070      1080      1090      1100      1110      1120
M CAAGCGCGATGGGGCGATATGGACCTGTCTGCAGTTTGTGAGTACCAGTTGGAACAGATCCAGCAAGTGT
::      :::::      ::      :      ::::      :      ::::
H CA-----TGGGGC-----CC--C-----ACCA-----C---TCCA-----
770

1130      1140      1150      1160      1170      1180      1190
M TTGAGGTCCTACAAGGAGTACAGTGAGCAAGCCAGAAAGTGGCCCCGTATACTGACCCGGTACCCAG
::::      ::      :::::      :::::      ..      ::      :      ::      :      ::      :
H -TGAAG-----ACA--GAGTAC-----CTGGCC---TTTGGCTCAACGAACCTCACTTTGTA---GG
790      800      810      820      830

1200      1210      1220      1230      1240      1250      1260
M CCCTCGGCCTGGTTCGTGTATCAACAACACTGGCACCCGAGACAATGGCTACACCAGTTCCTGGAAC TGCCG
:      ::      :::::      :::::      :::::      ::      ::      :      ::      :      ::
H C--TCTGCCTA-----TGTA-C-----CTGA-----GAGT-GTGGGCAGCTTCA---CGGGGGACGAC--
840      850      860      870      880

1270      1280      1290      1300      1310      1320      1330
M GACAACACCCCTCAACTTCATCAAGAAGCACCCCTGATGGAGAGACCAGGTGAAGCCTCGGTTGGGCCGCC
:::::      .      :      :::::      :::::      :::::      :      :::::      :      ::
H GACAAGGTCTACTTCTTCTCAGGGAGC-----GGGC--AGTGGAGTC-CGA-----
890      900      910      920

1340      1350      1360      1370      1380      1390      1400
M CCCTACTTGTGAAGAAGAACACTAACTTCACACACGTGGTGGCCGACAGGGTCCAGGGCTTGATGGTGC
:::::      ::      :      :      ::      :::::      ::      :      ::      :      ::
H --CTGCTA-----TGC--CGAGCAGGTGGTGGC-----TC-----GTGTGGC
930      940      950

```

Fig. 21L

Sequence alignment

```

1410      1420      1430      1440      1450      1460      1470
M CACCTATACAGTGTGTTTCATTGGTACAGGAGATGGCTGGCTGCTGAAGGCTGTGAGCCTGGGGCCCTGG
:  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
H C--CGTGTCTG-----CAAGGG--C--GATATGGGGGC-----GCA-----C--GGACCCCTG-
960      970      980      990

1480      1490      1500      1510      1520      1530      1540
M ATCCACATGGTGGAGGAACTGCAGGTGTTTGACCAGGAGCCAGTGGAAAGTCTGTGCTGTCTCAGAGCA
::  :::::  ::  :::::  .  :::::  :::::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
H -----GAGGAA-----GTG----GACCACGTTCCCTG----AAGGC----GCGG---CTG-GCA
1000      1010      1020      1030

1550      1560      1570      1580      1590      1600      1610
M AGAAGGTGCTCTTTGCTGGCTCCCGCTCTCAGCTGGTTTCAGCTGTCTCTGGCCGACTGCACAAAGTACCG
:::::  ::  :::::  ::  :::::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  ::
H -----TGCTCT-----GC-CCCGAACT-GGCAG-CTCTACT-TCA---ACCAGCTGCA---GG---CG
1040      1050      1060      1070      1080

1620      1630      1640      1650      1660      1670      1680
M TTTCTGTAGACTGTGTCCTGGCCAGGGACCCCTTACTGTGCCTGGAATGTCAACACCAGCCGCTGTGTG
.:  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
H ATGC-----ACA---CCCTG--CAGGACACCT-----CCTGGCA---CAACACCACCTTCTTTGGG
1090      1100      1110      1120      1130

1690      1700      1710      1720      1730      1740      1750
M GCCACCACCAAGTGTGCTCGGCTCGGGGTCCCTTTCTGTGTCCAACATGTGGCGAACTTGGACACTTCAAAGATGT
:  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
H GTTT--TTCAA-----GCACAGTGG-----GGT--GACATGTACCTGTC---GGC-CATCTG---TGA
1140      1150      1160      1170

```

Fig. 21M

```

1760      1770      1780      1790      1800      1810      1820
M GTAACCAGTATGGCATTAATAAAGTCAGATCTATTCCCAAGAACAATCACCGTTGTGTCAGGCACAGACCT
  :: ::::: ::::      ::::      ::::      ::::      ::::      ::::
H GTA-CCAGT-TGG-----AAG--AGATC-----CAGCG--GGTGTTTGAGG-----
1180      1190      1200      1210

1830      1840      1850      1860      1870      1880      1890
M GGTCCTACCCCTGCCACCTCTCGTCCAATTGGCCCATGCCCACTGGACCTTCGGAAGCCAGGACCTGCCT
  ::      ::::: :::::      :::::      ::::      :::::      :::::
H -----GCC-----CCTATAAGGA--GTACC---ATGA-----GGAAGC-----CCA
1220      1230      1240

1900      1910      1920      1930      1940      1950      1960
M GCAGAAACAACCTGGCTCCTTTCTTTATGACACGGGACTCCAGGCGCTGGTGTGATGGCCGCACAGTCCC
: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
H GAAGTGGGACC--GCTAC--ACT---GACCCCTGTAC--CCAGGCCCTGGTTGTGATGGCTGCCCAAGCCCC
1250      1260      1270      1280      1290      1300

1970      1980      1990      2000      2010      2020      2030
M GTCACCTCTGGACCCCTATCGTTGCTATTTCAGAGGAGCAGGGACAAGACTGGCTGCAGAAAGCTACCTTGT
: ::      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
H GCCATGCCGGGGCCTACCACTGCTTTTCAGAGGAGCAGGGGCGCGGCTGGCTGCTGAAGGCTACCTTGT
1310      1320      1330      1340      1350      1360      1370

2040      2050      2060      2070      2080      2090      2100
M TGCTGTCTGTCGGCCGGCTCGTCTGGTGACACTGGAGGCACGGGCTCCCTTGAAAAACCTGGGGCTCGTGTGG
: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
H GGCTGTCTGGCAGGCCCGTCGGTGACCTTGGAGGCCCGGGCCCCCTGAAAAACCTGGGGCTGGTGTGG
1380      1390      1400      1410      1420      1430      1440

```

Fig. 21N

```

2110      2120      2130      2140      2150      2160      2170
M CTCGCTGTGTGGCCCTGGGGGCTGTGTGCCTGGTGTCTGTCTATCGTCCGCCGGCGAC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H CTGGCGGTGTGGCCCTGGGGGCTGTGTGCCTGGTGTCTGTCTATTCGCGCCGGCGGC
1450      1460      1470      1480      1490      1500      1510

2180      2190      2200      2210      2220      2230      2240
M TTCGAGAAGAGCTAGAAAAGGTGCCAAGCATCTGAGAGGACACTGGTGATCCCTTGGAAC TGCCCAA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H TCGGGGAAGAGCTGGAGAAAAGGGGCCAAGCTACTGAGAGGACCTTGGTGATCCCTGGAGCTGCCCAA
1520      1530      1540      1550      1560      1570      1580

2250      2260      2270      2280      2290      2300      2310
M GGAGCCTGCCAGTCCCCCTTCCGTCTCCGCCCCGAAACTGATGAGAAACTTTGGGATCCTGTGCGGTAC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GGAGCCCACCAAGTCCCCCTTCCGGCCCTGTCTGAACCAAGATGAGAAACTTTGGGATCCTGTGCGGTAC
1590      1600      1610      1620      1630      1640      1650

2320      2330      2340      2350      2360      2370      2380
M TACTATTCGGATGGCTCTCTCAAGATTGTGCTGCACGCCCCGGTGCCAGCCTGGGGGTGGGCCCCCTT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H TACTATTCAGATGGCTCCCTTAAGATAGTACCTGGGCATGCCCGGTGCCAGCCCGGTGGGGGCCCCCTT
1660      1670      1680      1690      1700      1710      1720

2390      2400      2410      2420      2430      2440      2450
M CCCCACCTCCTGGCATACCTGGCCAGCCTCTGCCTTCTCCAACCTCGGCTCCACCTAGGAGTGGTCGGAA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H CGCCACCTCCAGGCATCCCAGGCCAGCCTCTGCCTTCTCCAACCTCGGCTTCACCTGGGGGTGGCGGAA
1730      1740      1750      1760      1770      1780      1790

```

Fig. 210

	2460	2470	2480	2490	2500	2510	2520
M	CTCAAATGCCAATGGTTATGTGCGTTTACAGTTGGCGGAGAGACCAGAGAGATCTGGGCACCCACTG						
	:::::::::::::::	::::::	::::::	::::::	::::::	::::::	::::::
H	CTCAAATGCCAATGGTTACGTGCGCTTACAAC TAGGAGGGAGAGACC GGGAGGCTCGGGCACCCCCCTG						
	1800	1810	1820	1830	1840	1850	1860

	2530	2540	2550	2560	2570	2580	2590
M	CCTGAGCTCGGGATGAATTACGACGAAACTACAACAGCCAGCCGCTGCCTGACTCCAACCAGAGG						
	:::::::::::::::	:: ::	:::::::::::::::	:::::::::::::::	:::::::::::::::	:::::::::::::::	::::
H	CCTGAGCTCGGGATGAACTGAGACGCAAACTGCAGCAACGCCAGCCACTGCCGACTCCAACCCCAGG						
	1870	1880	1890	1900	1910	1920	1930

	2600	2610	2620	2630	2640	2650
M	AGTCTTCAGTATGAGGGACCCCCACCTCAT	TGGCGGGGGGGTCTCATGGAGTGCA-CTCTTAA				
	::::::::::	::::	::	::::::::::	::::::::::	:: ::
H	AGTCATCAGTATGAGGGGAACCCC-ACCGCGTCGGCGGAAG-----CGTGGAGGTGTAGCTCCTA-					
	1940	1950	1960	1970	1980	1990

	2660	2670	2680	2690	2700	2710	2720
M	CTTTGCACAGGCAC	AGCTACCTCAGG	ACATGCAGGGCA	CTTGCTCTGCCT	GGGACACACTGCC		
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
H	CTTTGCACAGGCAC	AGCTACCTCAGG	ACATGCAGGGCA	CTTGCTCTGCCT	GGGACACACTGCC		
	2000	2010	2020	2030	2040	2050	2060

	2730	2740	2750	2760	2770	2780	2790
M	CATCATTTGCCCCGGCCGTAGGACCTGCTC-----AGCATGGGCACCTGCCACTTGGTGTGGCTCACCAGG						
	:: ::	:: ::	:: ::	:: ::	:: ::	:: ::	:: ::
H	CAGCACCCACCCGGCCATGAGGACCTGCTCTGCTCAGCACGGGCACCTGCCACTTGGTGTGGCTCACCAGG						
	2070	2080	2090	2100	2110	2120	2130

Fig. 21P

```

2800      2810      2820      2830      2840      2850      2860
M ACTTCAGCCCTCACAGGAGACA-CACCCCTCCTCT--GTGAATTTGAGACATGTGGGACCCAGCAGCCAAA
.. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GCACCAAGCCTCGCAGAAGGCATCTTCCTCCTCTCTGTGAATCACAGACACGCGGACCCAGCCGCCCCAAA
2140      2150      2160      2170      2180      2190      2200

2870      2880      2890      2900      2910      2920
M ACTTTGCAAGGAAGAGGTTTCAAGATGTGGCGGTGTTGTGCAT--ATATGTTGGTATGCATGTGGAA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H ACTTTTCAAGGCAGAAAGTTTCAAGATGTGTGTTGTCTGTATTTGCACATGTGTTGTGTGTGTGTAT
2210      2220      2230      2240      2250      2260      2270

2930      2940      2950      2960      2970      2980      2990
M GAATGTGTGTGTGTGTG--TGTTGTGTAACCTTTCCTGTCTCTATCACGCTTTCCTTGGCCTGG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GTGTGTGTGCACGCGCGTGTGGCCTTGTGGCATAAGCCTTCCTGTTCTGTCAAGTCTTCCCTTGGCCTGG
2280      2290      2300      2310      2320      2330      2340

3000      3010      3020      3030      3040      3050      3060
M GGTCCCTCCTGTTGAGTCTTTGGAGCTATGAAGGGGAAGGGGTCATAGCACCTTTGCTTCTCCTACCCCC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H G-TCCTCCTGGT-GAGTCATTGGAGCTATGAAGGGGAAGGGG-TCGTATCACCTTTGTCTCTCCTACCCCC
2350      2360      2370      2380      2390      2400      2410

3070      3080      3090      3100      3110      3120      3130
M AGCTGTCCCAAGCTTTGGGGCAGTGATGTACATACGGGGAAGGGAAGACAGGTTGTGTACCCCTTTTG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H A-CTGCCCCCGAG-TGTCGGGCAGCGATGTACATATGGAGGTGGGGTGGACAGGTTGTGTGCCCTTCAG
2420      2430      2440      2450      2460      2470      2480

```

Fig. 21Q

```

3140      3150      3160      3170      3180      3190      3200
M GGGAGTGGGACTCGGGGTGGGCCTAGCCCTGCTCCTAGGGCTGTGAATGTTTTCAGGGCGGGGTT
      .:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
H AGGAGTGCAGGGCT-TGGGGTGGGCCTAGTCTGCTCCTAGGGCTGTGAATGTTTTCAGGGTGGGGGA
2490      2500      2510      2520      2530      2540      2550

3210      3220      3230      3240      3250      3260      3270
M GGGGTGGAGATGGAACCTCCTGC--TTCAGGGGAGGGTGGCAGGGCCTCCCACCTGCCCTCCGGG
      .:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
H GGG-----AGATGGAGCCTCCTGTGTGTTTGGGGGAAGGTGGGTGGGCCTCCCACCTTGGCCCCGGGG
2560      2570      2580      2590      2600      2610

3280      3290      3300      3310      3320      3330
M TTCGGTGGTATTTTATATTTCGGCTCTTC-TG-ACAGGCTGGGAAGG--TTGTGGGGAGGAAGGG
      .:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
H TTCAGTGGTATTTTATACTTGCCCTTCTTCCTGTACAGGGCTGGGAAAGGCTGTGTGAGGGGAGAAAGG
2620      2630      2640      2650      2660      2670      2680

3340      3350      3360      3370      3380      3390      3400
M AGGAGTGGGCATGCTATGGATACTGGCCCTATCCTCCTGCTCTGGGAAAAGGGCT---AACAGTGA
      .:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
H AGAGGTGGGCCTGCTGTGGACAAATGCATACTCTCTCCAGCCCTAGGAGGAGGCTCCTAACAGTGA
2690      2700      2710      2720      2730      2740      2750

3410      3420      3430      3440      3450      3460      3470
M ACTTATTGTGTCCCCACATATTTATTGTTGTAAATATTTGAGTATTTTATATTGACAAATAAATGGA
      .:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
H ACTTATTGTGTCCCCCGGTATTTATTGTTGTAAATATTTGAG-ATTTTATATTGA-----
2760      2770      2780      2790      2800      2810

```

Fig. 21R

GTGACCCACGCTCCGCGGACGCGTGGGCGCGCGGGGCCATCCAGACCCCTGCGGAGAGCGGCGGAGCGTCGCC	79
GAGGTTTGAGGCGCGGAGACCGAGGGCCTGGCGGCCGAAGAACCGCCCCCAAGAGACCTCTGGCCCCGGGGCTGC	158
TGGAACATGTGCGGGGGACACAGTTTGTGACAGTTGCCAGACT ATG TTT ACG CTT CTG GTT CTA CTC	228
S Q L P T V T L G F P H C A R G P K A S	28
AGC CAA CTG CCC ACA GTT ACC CTG GGG TTT CCT CAT TGC GCA AGA GGT CCA AAG GCT TCT	288
K H A G E E V F T S K E E A N F F I H R	48
AAG CAT GCG GGA GAA GAA GTG TTT ACA TCA AAA GAA GAA GCA AAC TTT TTC ATA CAT AGA	348
R L L Y N R F D L E L F T P G N L E R E	68
CGC CTT CTG TAT AAT AGA TTT GAT CTG GAG CTC TTC ACT CCC GGC AAC CTA GAA AGA GAG	408
C N E E L C N Y E E A R E I F V D E D K	88
TGC AAT GAA GAA CTT TGC AAT TAT GAG GAA GCC AGA GAG ATT TTT GTG GAT GAA GAT AAA	468
T I A A F W Q E Y S A A K G P T T K S D G N	108
ACG ATT GCA TTT TGG CAG GAA TAT TCA GCT AAA GGA CCA ACC ACA AAA TCA GAT GGC AAC	528

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Fig. 22A

R E K I D V M G L L T G L I A A G V F L 128
 AGA GAG AAA ATA GAT GTT ATG GGC CTT CTG ACT GGA TTA ATT GCT GCT GGA GTA TTT TTG 588

 V I F G L L G Y Y L C I T K C N R L Q H 148
 GTT ATT TTT GGA TTA CTT GGC TAC TAT CTT TGT ATC ACT AAG TGT AAT AGG CTA CAA CAT 648

 P C S S A V Y E R G R H T P S I I F R R 168
 CCA TGC TCT TCA GCC GTC TAT GAA AGG GGC AGG CAC ACT CCC TCC ATC ATT TTC AGA AGA 708

 P E E A A L S P L P P S V E D A G L P S 188
 CCT GAG GAG GCT GCC TTG TCT CCA TTG CCG CCT TCT GTG GAG GAT GCA GGA TTA CCT TCT 768

 Y E Q A V A L T R K H S V S P P P Y P 208
 TAT GAA CAG GCA GTG GCG CTG ACC AGA AAA CAC CAC AGT GTT TCA CCA CCA CCA CCA TAT CCT 828

 G H T K G F R V F K K S M S L P S H * 227
 GGG CAC ACA AAA GGA TTT AGG GTA TTT AAA AAA TCT ATG TCT CTC CCA TCT CAC TGA 885

 CTACCTTGTCATTTGGTATAAGAAATTTGTGTTATTTGATAGCCGGCATGGTGGCTCATGCTGTAATCCAGCAC 964

 TTTGGAGGCCAGGAGTTCGAGACCAGCCTGGCCAAACATGGTGAAACCCGGTCTCTACTAAAAAATTCAAAAATTACCTA 1043

 GCGTCATGGGGCATGCCCTGTAGTCCCACCTACTTGGAGGCTGAAGCAGGAGAAATTGCTCGAACCTGGGAGGCAGAGG 1122

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Fig. 22B

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Fig. 22C

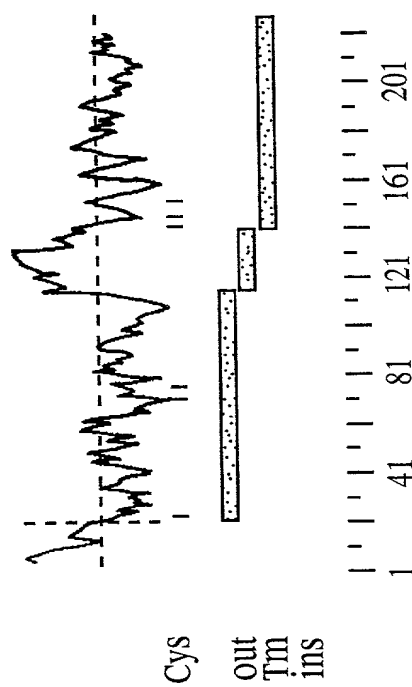


FIG. 22D

GTCGACCCAC	CGGTCCGCTG	CGTTCTCACC	CCTGGACCAC	CCTGGGAGAA	CAGTTGACCG	60
AAGTTTGTTT	GGCAGTTGCT	GCTGGACT	ATG TTT CTG	CTT CTG	GTA CTC	112
	Met	Phe	Leu	Leu	Val	Leu
	1					5
AGC CAG CTG	CCC AGA CTT	ACC CTC	GCG GTT	CCT CAT	ACA AGA AGC CTA	160
Ser Gln	Leu Pro	Arg Thr	Leu Ala	Val Pro	His Thr	Arg Ser
	10					20
AAG AAT TCT	GAA CAT GCC	CCA GAA	GGA GTC	TTT GCA	TCA AAA AAA GCA	208
Lys Asn	Ser Glu	His Ala	Pro Glu	Gly Val	Phe Ala	Ser Lys
	25					40
						35
GCA AGC ATC	TTT ATG CAC	CGT CGC	CTC CTA	TAC AAT	AGA TTT GAT TTA	256
Ala Ser	Ile Phe	Met His	Arg Arg	Leu Tyr	Asn Arg	Phe Asp
	45					55
GAA CTC TTC	ACT CCC	GCG AAC	CTG GAG	AGA GAG	TGC TAT	GAG GAG
Glu Leu	Phe Thr	Pro Pro	Gly Asn	Leu Glu	Arg Cys	Tyr Glu
	60					70
						65
TGT AGT TAT	GAA GAA	GCC AGA	GAG ATC	CTC GGG	GAC AAC	GAA GAA
Cys Ser	Tyr Glu	Glu Glu	Ala Arg	Glu Ile	Leu Gly	Asn Glu
	75					85
						80

Fig. 22E

ATC ACA TTC TGG CGG GAA TAT TCA GTC AAA GGA CCA ACC ACA AGA TCA	400
Ile Thr Phe Trp Arg Glu Tyr Ser Val Lys Gly Pro Thr Thr Arg Ser	
90	
GAT GTC AAC AAA GAG AAA ATT GAT GTT ATG GGC CTT CTG ACT GGC TTA	448
Asp Val Asn Lys Glu Lys Ile Asp Val Met Gly Leu Thr Gly Leu	
105	
110	
115	
120	
ATT GCG GCT GGA GTA TTC TTG GTT TTT GGC TTA CTT GGT TAC TAT	496
Ile Ala Ala Gly Val Phe Leu Val Val Phe Gly Leu Gly Tyr Tyr	
125	
130	
135	
CTG TGT ATC ACC AAG TGT AAT AGG CAG CCA TAT CAA GGT TCT TCA GCT	544
Leu Cys Ile Thr Lys Cys Asn Arg Gln Pro Tyr Gln Gly Ser Ser Ala	
140	
145	
150	
GTC TAC ACA AGA AGG ACC AGG CAC ACA CCG TCC ATC ATT TTC AGA ACC	592
Val Tyr Thr Arg Arg Thr Arg His Thr Pro Ser Ile Ile Phe Arg Thr	
155	
160	
165	
CAT GAG GAA GCT GTC TTG TCT CCA TCG TCA TCC TCA GAG GAC GCG GGA	640
His Glu Glu Ala Val Leu Ser Pro Ser Ser Ser Ser Glu Asp Ala Gly	
170	
175	
180	

Fig. 22F

CTA CCT TCC TAT GAA CAG GCA GTA GCT CTG ACC AGA AAA CAC AGT GTC	688
Leu Pro Ser Tyr Glu Gln Ala Val Ala Leu Thr Arg Lys His Ser Val	200
185	190
TCA CCA CCA CCT CCA TAT CCT GGG CCA GCA AAA GGA TTT AGG GTA TTT	736
Ser Pro Pro Pro Tyr Pro Gly Pro Ala Lys Gly Phe Arg Val Phe	215
205	210
AAA AAG TCA ATG TCA CTC CCA TCT CAC TAAGCCCACC TTGCCGCCTT	783
Lys Lys Ser Met Ser Leu Pro Ser His	
220	225
GCTGTGGTCT GAATAATATG TTCTTCCTGA AACAAACAACA ACAAATAAT TTGCCTGTTC	843
AGCTTTTAT GACAAAGCAC AAGGAATAAA GGAACACTAT ATACAGAACA GAATTCACCA	903
CAGCCCCGCT TTCAGCTCTG CCCCCAAGTG GATTGCTGTC TTGGTAAGAG ACTTCTACCG	963
TGCTTCCTCG AAGTTAAGAA GAAAGTGCCT TTTTGCAATG TAAACTGTAC TGGTTCAAAC	1023
ATTCTTGCTA CAGCTAGGTA CCTATAATCC CCACCTTCAG GAGACTTAGG CGGGAGGGAT	1083
GAGAGTTCAA GGCCAGCCTG GGCCCTGTCA GGACGCTGTC TCAAAACAAA GTTTGTATC	1143
AATAGAATAA TTAGAATTAA CAAACTAGGA TTTTCAGTCT TAAGTCATGA TATTGGATCT	1203
TCTCTTCAGT AAGGTTTCTT TTTGGCTAGA AATACTTCAT AGAATTGAC ATTTTGGTAT	1263
ACATCTGTGG CCTTGATACA ATGACTTGAT TTTCTGTTT AATTAGTGCA GAGGATTCAG	1323
CAAATTGCA GGTCTTCATT TTGTTCCCTC GCTATCCATC GATCATGTTT CAGTGTATTA	1383
AGAGGAGTCA GCCAGGCGTG GTGGCCACAC CCTGTGATCC CAGCACTTAG GGGGCATAG	1443
GCAGGCAGAT CTCTGTGAGC TGAAGGACAG CCTGGCCTAC AAAGTCCAGG ACAACCCAGA	1503
CCACACAGAG AAACCTTGTC TTGAAAAACA AAACAAAAAC AAGAGAGAGA GAGAGAGAGA	1563

Fig. 22G

GAGAAAAGAG	ATGTCAAGAG	GTTTTTGTTT	TTTTTTTTTT	AAATTACTAT	TTATGGGCCT	1623
CAC TTGGAAA	AGTGCTTGCC	ATGCAAAATAG	AAGGACAGGA	GTTCAATCCT	CATTACCCAC	1683
ATT TGAACA	AATAACAAGA	AAAACAAAAC	AAAAAACCAA	AACAAACAAA	ATCTTGAGAA	1743
CTTGAGTGAA	TACCGGTAAC	CTCAGGGCTA	GGCACTGTAA	CTGAATCAGG	AGCCTCCAGA	1803
TCCAGGGGAAA	CGCTGTCTCA	ACAAATAAAT	AAATAAGTAA	GTCAGTGAGG	TGGTCTTTAA	1863
ACCCAGCACT	TGAGAGCCAA	AGCAGGCAG	AGCTCAGTGA	GTTGGAGACC	AGCCTGGTCT	1923
ACAAAGCAAG	TTCTAAGGGA	GCCAGGGCAC	AGAGAAACCC	TGTCTGAAGG	AAAAAATAAA	1983
AAAAAAAAG	GGCGGCCGC					2002

Fig. 22H

```

G      1  ATGTTTCTGCTTCTGGTGGTACTCAGCCAGCTGCCCAGACTTACCCTCGC  50
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
H      1  ATGTTTACGCTTCTGGTCTACTCAGCCAACTGCCACACAGTTACCCTGGG  50

G      51  GGTTCCTCAT...ACAAGAAGCCCTAAAGAATTCTGAACATGCCCCCAGAAG  97
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
H      51  GTTCCCTCATTGGCAAGAGAGGTCCAAAGGCTTCTAAGCATGCGGGAGAAG  100

G      98  GAGTCCTTGCATCAAAAAAGCAGCAAGCATCTTTATGCACCGTCGCCCTC  147
      |||  |||  |||||  |||  |||||  |||  |||  |||  |||  |||||
H     101  AAGTGTTTACATCAAAAGAAGAAGCAAACTTTTTCATACATAGACGCCCTT  150

G     148  CTATACAAATAGATTTGATTTAGAACTCTTCACTCCCCGGGAACCTGGAGAG  197
      ||  ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
H     151  CTGTATAATAGATTTGATCTGGAGCTCTTCACTCCCCGGCAACCTAGAAAAG  200

G     198  AGAGTGCTATGAGGAGTTCTGTAGTTATGAAGAAGCCAGAGAGATCCTCG  247
      |||||  |||||  ||  ||  |||||  |||||  |||||  |||||  |||||  |||||
H     201  AGAGTGCAATGAAGAACTTTGCAATTATGAGGAAGCCAGAGAGATTTTGTG  250

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Fig. 22I

G	248	GGGACAAACGAAAGAAATGATCACATTCTGGCGGGAATATTCAGTCAAAGGA	297
H	251	TGGATGAAGATAAAACGATTGCATTTTGGCAGGAATATTCAGCTAAAGGA	300
G	298	CCAACCACAAGATCAGATGTCAACAAGAGAAAATTGATGTTATGGGCCT	347
H	301	CCAACCACAATAATCAGATGGCAACACAGAGAAAATAGATGTTATGGGCCT	350
G	348	TCTGACTGGCTTAATTGCGGCTGGAGTATCTTGGTTTGGCTTAC	397
H	351	TCTGACTGGATTAAATGCTGCTGGAGTATTTGGTTATTTGGATTAC	400
G	398	TTGGTTACTATCTGTGTATCACCAAGTGTAATAGGCAGCCATATCAAGGT	447
H	401	TTGGCTACTATCTTTGTATCACTAAGTGTAATAGGCTACAACATCCATGC	450
G	448	TCCTTCAGCTGTCTACACAAGAAGGACCAGGCACACACCCGTCCATCATTTT	497
H	451	TCCTTCAGCCGTCATGAAAGGGG...AGGCACACTCCCTCCATCATTTT	497

Fig. 22J

```

G      498 CAGAAACCCATGAGGAAGCTGTCTTGTCTCCAT...CGTCATCCTCAGAGG 544
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
H      498 CAGAAACCTGAGGAGGCTGCCCTTGTCTCCATTGCCGCCCTTCTGTGGAGG 547

G      545 ACGCGGGACTACCTTCCTATGAACAGGCAGTAGCTCTGACCAGAAAACAC 594
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
H      548 ATGCAGGATTACCTTCTTATGAACAGGCAGTGGCGCTGACCAGAAAACAC 597

G      595 AGTGTCTCACCCACCACCTCCATATCCTGGGCCAGCAAAAGGATTTAGGGT 644
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
H      598 AGTGTTTCACCACCACCACCACCATATCCTGGGCACACAAAAGGATTTAGGGT 647

G      645 ATTTAAAAAGTCAATGTCACCTCCCATCTCAC 675
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
H      648 ATTTAAAAAATCTATGTCTCTCCCATCTCAC 678

```

Fig. 22K

```

G   1 MFLLLVLSQLPRLTLAVPH.TRSLKNSEHAPEGVFASKKAASIFMHRRL 49
H   1 MFTLLVLSQLPTVTLGPHCARGPKASKHAGEEVFTSKEEANFFIHRRL 50

G   50 LYNRFDELFTPGNLERECYEEFCSYEEAREILGDNEEMITFWREYSVKG 99
H   51 LYNRFDELFTPGNLERECNEELCNYYEAREIFVDEDKTIAFWQEYSAG 100

G   100 PTTRSDVNKEKIDVMGLLTGLIAAGVFLVFGLLGYLYLCITKCNRPYQG 149
H   101 PTKSDGNREKIDVMGLLTGLIAAGVFLVIFGLLGYLYLCITKCNRLQHPC 150

G   150 SSAVYTRRTRHTPSIIFRTHEEAVLSP.SSSSEDAGLPSYEQAVALTRKH 198
H   151 SSAVY.ERGRHTPSIIFRRP EEAAALSPLPSPVEDAGLPSYEQAVALTRKH 199

G   199 SVSPPPPPYPGPAKGFRVFKKMSMLPSH 225
H   200 SVSPPPPPYPGHTKGFRVFKKMSMLPSH 226

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Fig. 22L

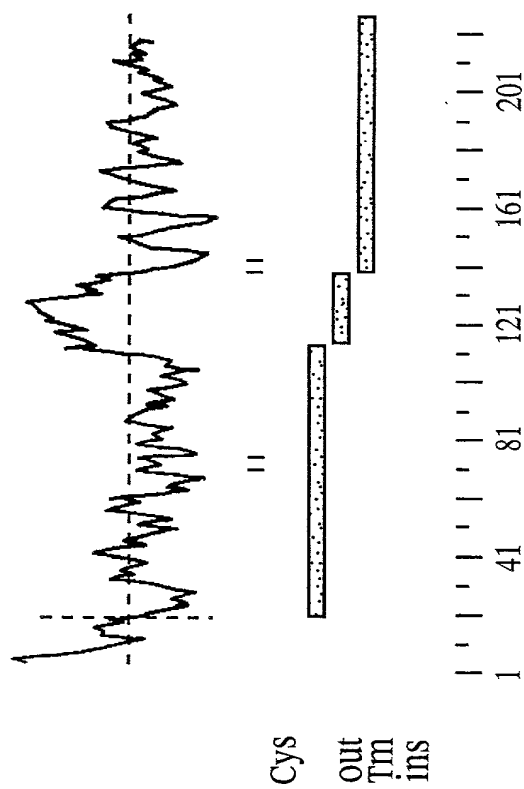


FIG. 22M

Sequence

T	Y	G	P	D	C	L	A	C	Q	G	G	S	Q	R	P	C	S	G	N	151
ACC	TAC	GGT	CCC	GAC	TGT	CTC	GCA	TGC	CAG	GGC	GGA	TCC	CAG	AGG	CCC	TGC	AGC	GGG	AAT	566
G	H	C	S	G	D	G	S	R	Q	G	D	G	S	C	R	C	H	M	G	171
GGC	CAC	TGC	AGC	GGA	GAT	GGG	AGC	AGA	CAG	GGC	GAC	GGG	TCC	TGC	CGG	TGC	CAC	ATG	GGG	626
Y	Q	G	P	L	C	T	D	C	M	D	G	Y	F	S	S	L	R	N	E	191
TAC	CAG	GGC	CCG	CTG	TGC	ACT	GAC	TGC	ATG	GAC	GGC	TAC	TTC	AGC	TCG	CTC	CGG	AAC	GAG	686
T	H	S	I	C	T	A	C	D	E	S	C	K	T	C	S	G	L	T	N	211
ACC	CAC	AGC	ATC	TGC	ACA	GCC	TGT	GAC	GAG	TCC	TGC	AAG	ACG	TGC	TCG	GGC	CTG	ACC	AAC	746
R	D	C	G	E	C	E	V	G	W	V	L	D	E	G	A	C	V	D	V	231
AGA	GAC	TGC	GGC	GAG	TGT	GAA	GTG	GGC	TGG	GTG	CTG	GAC	GAG	GGC	GCC	TGT	GTG	GAT	GTG	806
D	E	C	A	A	E	P	P	P	C	S	A	A	Q	F	C	K	N	A	N	251
GAC	GAG	TGT	GCG	GCC	GAG	CCG	CCT	CCC	TGC	AGC	GCT	GCG	CAG	TTC	TGT	AAG	AAC	GCC	AAC	866
G	S	Y	T	C	E	E	C	D	S	S	C	V	G	C	T	G	E	G	P	271
GGC	TCC	TAC	ACG	TGC	GAA	GAG	TGT	GAC	TCC	AGC	TGT	GTG	GGC	TGC	ACA	GGG	GAA	GGC	CCA	926
G	N	C	K	E	C	I	S	G	Y	A	R	E	H	G	Q	C	A	D	V	291
GGA	AAC	TGT	AAA	GAG	TGT	ATC	TCT	GGC	TAC	GCG	AGG	GAG	CAC	GGA	CAG	TGT	GCA	GAT	GTG	986

Fig. 23B

D E C S L A E K T C V R K N E N C Y N T 311
GAC GAG TGC TCA CTA GCA GAA AAA ACC TGT GTG AGG AAA AAC GAA AAC TGC TAC AAT ACT 1046

P G S Y V C V C P D G G G C F E E T E D A C V 331
CCA GGG AGC TAC GTC TGT GTG TGT CCT GAC GGC TTC GAA GAA ACG GAA GAT GCC TGT GTG 1106

P P A E A E A T E G E S P T Q L P S R E 351
CCG CCG GCA GAG GCT GAA GCC ACA GAA GAA AGC CCG ACA CAG CTG CCC TCC CGC GAA 1166

D L * 354
GAC CTG TAA 1175

TGTGCCGGACTTACCCCTTTAAATTATTCAGAAGGATGTCCCGTGGAAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGT 1254

GGACAGCGCGGGGAGAGGCTGCCCTGCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGTGTG 243/361 1333

TTCTTAAACAGACTTGTATATTTTGATACAGTTCTTTGTAAATAAAATTGACCATTTGTAGTAATCAAAAAAAAAAAAA 1412

AAAAAGGCGCGCGCTAGAC 1432

Fig. 23C

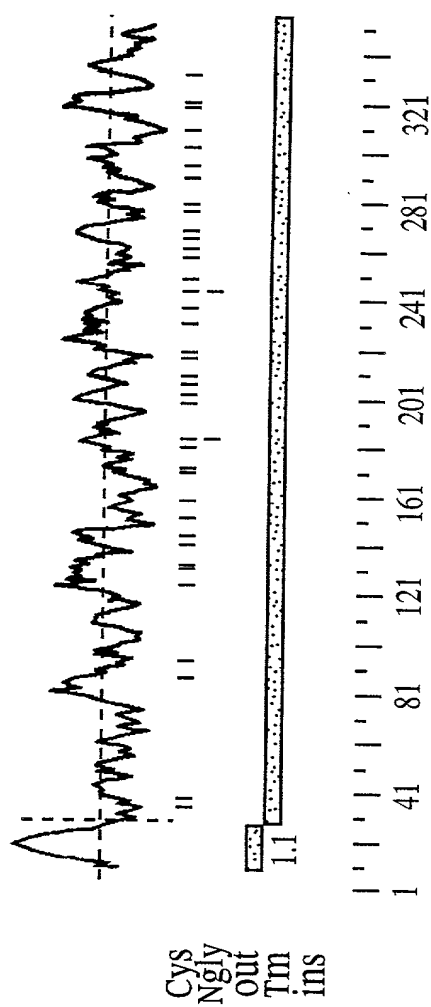


FIG. 23D

Fig. 23E

```

10      20      30      40      50
C  --GTAGCCGGG--GGAACGGC-CGGC-----GCGCTTG-----CCGGTGGCGGAGCGGAGACT-CCACA
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H  ACGCGTCCGCACANGCCGGCGGCTGGGAGCGGGTGGGCGGCCGGAGCGCGGAGCAGCAGCAGCGCCGCA
      10      20      30      40      50      60      70

      60      70      80      90      100      110
C  G---CAGTT-CTC-TGCCG-GTCG-CCCGCGAGTGC-ACCCGCCCATGCACCTGCCGC-CCGCTGCCGCAG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H  GGACCTGGAGCTCCGGCTGCGTCTTCCGC-AGCGCTACCCGCCCATGCGCCTGCCGCGCCG-GGCCGCGC
      80      90      100      110      120      130

      120      130      140      150      160      170      180
C  TCGGGCT---GCTACTGCTGCTGCCGCCCTCCCGCGCGGTGGCCTCCCGAAGCCGACAAATGTGCCA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H  TGGGGCTCCTGCCGCTTCTGCTGCTGCTGCCGCCCGCGCGGAGGCCCAAGAACCGACGCCCTGCCA
      140      150      160      170      180      190      200

      190      200      210      220      230      240      250
C  GAGGTGCCGGCGCTGGTGACAAAGTTCAACCAGGGGATGGCCCAACACGGCCAGGAAGAAATTCGGCGGC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H  CCGGTGCCGGGGCTGGTGACAAAGTTAAACCAGGGGATGGTGACACCGCAAGAAAGAACTTTGGCGGC
      210      220      230      240      250      260      270

```

Fig. 23F

```

260      270      280      290      300      310      320
C  GGCAACACGGCGTGGAGGAGAAAGAGTCTGTCCAAGTACGAATTCAGTGAGATTCGGCTCTGGAGATT
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
H  GGAAACACGGCTTGGAGAGAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTCGCCCTGCTGGAGATCC
280      290      300      310      320      330      340

330      340      350      360      370      380      390
C  TGGAGGGCCTGTGTGACAGCAACGACTTTGAATGCAACCAACT-CTTGGAACAGCATGAGGAGCAGCTAG
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
H  TGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGC-GCAGGAGGAGCACCTGG
350      360      370      380      390      400      410

400      410      420      430      440      450      460
C  AGGCCTGGTGGCAGACACTGAAGAAGGAGTGCCCTAACCTATTGAGTGGTTCGTGTACACACACTGAA
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
H  AGGCCTGGTGGCTGCAGCTGAAGAGCGGAATATCCTGACTTATTCGAGTGGTTTGTGTGAAGACACTGAA
420      430      440      450      460      470      480

470      480      490      500      510      520      530
C  AGCATGCTGTCTTCCAGGCACCTATGGGCCAGACTGTGAGGAATGCCAGGTGGGTCTCAGAGGCCCTGT
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
H  AGTGTGCTGTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGCCAGGGCGGATCCCAGAGGCCCTGC
490      500      510      520      530      540      550

```

Fig. 23G

Fig. 23H

```

      820      830      840      850      860      870      880
C  GCAATGTACAGTACTGTGAAAAATGTCAACGGCTCCTACACATGTGAAGAGTGTGATTCTACCTGTGTGGG
   :: :: :::::::::::::: :: :::::::::::::: :::::::::::::: :: ::::::::::::::
H  GCGCTGCGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTGGG
   840      850      860      870      880      890      900

      890      900      910      920      930      940      950
C  CTGCACAGGAAAAGGCCAGCCAATTGTAAAGAGTGTATCTCTGGCTACAGCAAGCAGAAAAGGAGAGTGT
   :::::::::::::: :: :::::::::::::: :::::::::::::: :: ::::::::::::::
H  CTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGAGCACGGACAGTGT
   910      920      930      940      950      960      970

      960      970      980      990      1000      1010      1020
C  GCAGATATAGATGAATGCTCATTAGAAACAAAGGTGTGTAAGAAAGGAAAATGAGAACTGCTACAATACTC
   :::::::::::::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
H  GCAGATGTGGACGAGTGCTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACGAAAACTGCTACAATACTC
   980      990      1000      1010      1020      1030      1040

      1030      1040      1050      1060      1070      1080      1090
C  CAGGAGCTTTGTCTGCGTGTGTCCGGAAGGTTTCGAGGAAGACAGAAAGATGCTTGTGTACAGACAGCAG
   :::::::::::::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
H  CAGGAGCTACGTCTGTGTGTCTGACGGCTTCGAAGAA-ACGGAAGATGCCTGTGTGCCCCCGGCAG
   1050      1060      1070      1080      1090      1100      1110

```

Fig. 23I

```

1100      1110      1120      1130      1140      1150
C AAGCGAAGTGCAGAGGAAAGT--CCC-ACACAGCCACCCCTCCCATGAGGATTTGTGACGGGCATCCAG
  :: :::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
H AGGCTGAAGCCACAGAGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGA-----CCTG
1120      1130      1140      1150      1160      1170
1160      1170      1180      1190      1200      1210      1220
C GTTCAGAAGCTGGACTCTCACCCCTTTTAAAGTTATTGAGAGGACATCCTATAGAAAATGTGCCCCATGGAC
  : : :::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
H --TAATGTGCCGGACTT--ACCCCTTTAAATTATTTCAGAAAGGATGTCCCGTGGAATAATGTGCCCCCTGAGGA
1180      1190      1200      1210      1220      1230

1230      1240      1250      1260      1270      1280      1290
C ATCAACCCCATTTCTCCAGGAAGTTTGG-AGGAAGAAGCTGCCCTGCTTTGAAACAGTAGATACACTCATT
  . : : : : : :::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
H TGCCGCTCTC----CTGCAGTGGACAGCGGCGGAGAGGCTGCCCTGCTCTCTAACGGTTGATTCTCATTT
1240      1250      1260      1270      1280      1290      1300
1300      1310      1320      1330      1340      1350      1360
C GGCCCTTTAAACGCTGCATTTCTTGTTGGTTCTTTAAACAGATTTCGTATATTTTGATACTGTTCTTTATA
  : ::::: : : ::::: ::::: ::::: ::::: ::::: ::::: :::::
H GTCCCTTAAACA-GCTGCATTTCTTGTTGTTCTTTAAACAGACTTGTATATTTTGATACAGTCTTTGTA
1310      1320      1330      1340      1350      1360      1370

1370      1380      1390
C ATAAAAATTGATCATTTGAAGGTCACCAGGAA-----CA-----
  ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
H ATAAAAATTGACCATTTGTAGGTAATCAAAAAAAGGCGCGCGCTAGAC
1380      1390      1400      1410      1420      1430

```

Fig. 23J

GTCGACCCACGCGTCCGTCTGCGGGCCCCAGCCCTCTCCTCAGCTCGCGCAGTCTCCGCCGCGAGTCTCAGCTGCAGCTG	79
CAGGACTGAGCCCGTGACCCCGGAGGAGACCCCGGAGGAGCGACAAACTTCGCAGTGCCCGGACCCCAACCCAGCCCT	158
<div>M</div> <div>A</div> <div>Q</div> <div>L</div> <div>F</div> <div>L</div> <div>P</div> <div>L</div> <div>L</div> <div>A</div> <div>A</div> <div>L</div> <div>V</div> <div>L</div> <div>A</div> <div>Q</div>	16
GGTAGCCTGCAGC ATG GCC CAG CTG TTC CTG CCC CTG CTG GCA GCC CTG GTC CTG GCC CAG	220
<div>A</div> <div>P</div> <div>A</div> <div>A</div> <div>L</div> <div>A</div> <div>D</div> <div>V</div> <div>L</div> <div>E</div> <div>G</div> <div>D</div> <div>S</div> <div>S</div> <div>E</div> <div>D</div> <div>R</div> <div>A</div> <div>F</div> <div>R</div>	36
GCT CCT GCA GCT TTA GCA GAT GTT CTG GAA GGA GAC AGC TCA GAG GAC CGC GCT TTT CGC	280
<div>V</div> <div>R</div> <div>I</div> <div>A</div> <div>G</div> <div>D</div> <div>A</div> <div>P</div> <div>L</div> <div>Q</div> <div>G</div> <div>V</div> <div>L</div> <div>G</div> <div>G</div> <div>A</div> <div>L</div> <div>T</div> <div>I</div> <div>P</div>	56
GTG CGC ATC GCG GGC GAC GCG CCA CTG CAG GGC GTG CTC GGC GGC GGC CTC ACC ATC CCT	340
<div>C</div> <div>H</div> <div>V</div> <div>H</div> <div>Y</div> <div>L</div> <div>R</div> <div>P</div> <div>P</div> <div>P</div> <div>S</div> <div>R</div> <div>R</div> <div>A</div> <div>V</div> <div>L</div> <div>G</div> <div>S</div> <div>P</div> <div>R</div>	251/361
TGC CAC GTC CAC TAC CTG CTG CCG CCA CCG CCG AGC CGC CGG GCT GTG CTG GGC TCT CCG CGG	76
<div>V</div> <div>K</div> <div>W</div> <div>T</div> <div>F</div> <div>L</div> <div>S</div> <div>R</div> <div>G</div> <div>R</div> <div>E</div> <div>A</div> <div>E</div> <div>V</div> <div>L</div> <div>V</div> <div>A</div> <div>R</div> <div>G</div> <div>V</div>	400
GTC AAG TGG ACT TTC CTG TCC TCC CGG GGC CGG GAG GCA GAG GTG CTG GTG GCG GGA GTG	96
<div>R</div> <div>V</div> <div>K</div> <div>V</div> <div>N</div> <div>E</div> <div>A</div> <div>Y</div> <div>R</div> <div>F</div> <div>R</div> <div>V</div> <div>A</div> <div>L</div> <div>P</div> <div>A</div> <div>Y</div> <div>P</div> <div>A</div> <div>S</div>	460
CGC GTC AAG GTG AAC GAG GCC TAC CGG TTC CGC GTG GCA CTG CCT CCG TAC CCA GCG TCG	116
<div>L</div> <div>T</div> <div>D</div> <div>V</div> <div>S</div> <div>L</div> <div>A</div> <div>L</div> <div>S</div> <div>E</div> <div>L</div> <div>R</div> <div>P</div> <div>N</div> <div>D</div> <div>S</div> <div>G</div> <div>I</div> <div>Y</div> <div>R</div>	520
CTC ACC GAC GTC TCC CTG GCG CTG AGC GAG CTG CGC CCC AAC GAC TCA GGT ATC TAT CGC	136
	580

Fig. 24A

C	E	V	Q	H	G	I	D	S	S	D	A	V	E	V	K	V	K	G	156
TGT	GAG	GTC	CAG	CAC	GGC	ATC	GAT	GAC	AGC	AGC	GCT	GTG	GAG	GTC	AAG	GTC	AAA	GGG	640
V	V	F	L	Y	R	E	G	S	A	R	Y	A	F	S	S	G	A	Q	176
GTC	GTC	TTT	CTC	TAC	CGA	GAG	GGC	TCT	GCC	CGC	TAT	GCT	TTC	TTT	TCT	GGG	GCC	CAG	700
E	A	C	A	R	I	G	A	H	I	A	T	P	E	Q	L	Y	A	Y	196
GAG	GCC	TGT	GCC	CGC	ATG	GGA	GCC	CAC	ATC	GCC	ACC	CCG	GAG	CAG	CTC	TAT	GCC	TAC	760
L	G	G	Y	E	Q	C	D	A	G	W	L	S	D	Q	T	V	R	P	216
CTT	GGG	GGC	TAT	GAG	CAA	TGT	GAT	GCT	GGC	TGG	CTG	TCG	GAT	CAG	ACC	GTG	AGG	TAT	820
I	Q	T	P	R	E	A	C	Y	G	D	M	D	G	F	P	G	V	R	236
ATC	CAG	ACC	CCA	CGA	CGA	GAG	GCC	TGT	TAC	GGA	GAC	ATG	GAT	GGC	TTC	CCC	GGG	GTC	880
Y	G	V	V	D	P	D	D	L	Y	D	V	Y	C	Y	A	E	D	L	252/361
TAT	GGT	GTG	GTG	GAC	CCG	GAT	GAC	CTC	TAT	GAT	GTG	TAC	TGT	TAT	GCT	GAA	GAC	CTA	256
G	E	L	F	L	G	D	P	P	E	K	L	T	L	E	E	A	R	A	940
GGA	GAA	CTG	TTC	CTG	GGT	GAC	CCT	CCA	GAG	AAG	CTG	ACA	TTG	GAG	GAA	GCA	CGG	TAC	276
C	Q	E	R	G	A	E	I	A	T	T	G	Q	L	Y	A	A	W	D	1000
TGC	CAG	GAG	CGG	GGT	GCA	GAG	ATT	GCC	ACC	ACG	GGC	CAA	CTG	TAT	GCA	GCC	TGG	GAT	296
																			1060

Fig. 24B

Table 3: Continued

G	L	D	H	C	S	P	G	W	L	A	D	G	S	V	R	Y	P	I	V	316
GGC	CTG	GAC	CAC	TGC	AGC	CCA	GGG	TGG	CTA	GCT	GAT	GGC	AGT	GTG	CGC	TAC	CCC	ATC	GTC	1120
T	P	S	Q	R	C	G	G	G	L	P	G	V	K	T	L	F	L	F	P	336
ACA	CCC	AGC	CAG	CGC	TGT	GGT	GGG	GGC	TTG	CCT	GGT	GTC	AAG	ACT	CTC	TTC	CTC	TTC	CCC	1180
N	Q	T	G	F	P	N	K	H	S	R	F	N	V	Y	C	F	R	D	S	356
AAC	CAG	ACT	GGC	TTC	CCC	AAT	AAG	CAC	AGC	CGC	TTC	AAC	GTC	TAC	TGC	TTC	CGA	GAC	TCG	1240
A	Q	P	S	A	I	P	E	A	S	N	P	A	S	N	P	A	S	D	G	376
GCC	CAG	CCT	TCT	GCC	ATC	CCT	GAG	GCC	TCC	AAC	CCA	GCC	TCC	AAC	CCA	GCC	TCT	GAT	GGA	1300
L	E	A	I	V	T	V	T	E	T	L	E	E	L	Q	L	P	Q	E	A	396
CTA	GAG	GCT	ATC	GTC	ACA	GTG	ACA	GAG	ACC	CTG	GAG	GAA	CTG	CAG	CTG	CCT	CAG	GAA	GCC	1360
T	E	S	E	S	R	G	A	I	Y	S	I	P	I	M	E	D	G	G	G	253/361
ACA	GAG	AGT	GAA	TCC	CGT	GGG	GCC	ATC	TAC	TCC	ATC	CCC	ATC	ATG	GAG	GAC	GGA	GGA	GGT	416
G	S	S	T	P	E	D	P	A	E	A	P	R	T	L	L	E	F	E	T	1420
GGA	AGC	TCC	ACT	CCA	GAA	GAC	CCA	GCA	GAG	GCC	CCT	AGG	ACG	CTC	CTA	GAA	TTT	GAA	ACA	436
Q	S	M	V	P	P	T	G	F	S	E	E	E	G	K	A	L	E	E	E	1480
CAA	TCC	ATG	GTA	CCG	CCC	ACG	GGG	TTC	TCA	GAA	GAG	GAA	GGT	AAG	GCA	TTG	GAG	GAA	GAA	456
																				1540

Fig. 24C

E	K	Y	E	D	E	E	K	E	E	E	E	E	E	V	E	D	476
GAG	AAA	TAT	GAA	GAT	GAA	GAG	AAA	GAG	GAA	GAA	GAG	GAG	GAG	GAG	GAG	GAT	1600
E	A	L	W	A	W	P	S	E	L	S	S	P	G	P	E	A	496
GAG	GCT	CTG	TGG	GCA	TGG	CCC	AGC	GAG	CTC	AGC	AGC	CCG	GGC	CCT	GAG	GCC	1660
T	E	P	A	A	Q	E	K	S	L	S	Q	A	P	A	R	A	516
ACT	GAG	CCA	GCA	GCC	CAG	CAG	AAG	TCA	CTC	TCC	CAG	GCG	CCA	GCA	AGG	GCA	1720
P	G	A	S	P	L	P	D	G	E	S	E	A	S	R	P	P	536
CCT	GGT	GCA	TCA	CCA	CTT	CCT	GAT	GGA	GAG	TCA	GAA	GCT	TCC	AGG	CCT	CCA	1780
G	P	P	T	E	T	L	P	T	P	R	E	R	N	L	A	S	254/361
GGA	CCA	CCT	ACT	GAG	ACT	CTG	CCC	ACT	CCC	AGG	GAG	AGG	AAC	CTA	GCA	TCC	556
S	T	L	V	E	A	R	E	V	G	E	A	T	G	G	P	E	1840
TCC	ACT	CTG	GTT	GAG	GCA	AGA	GAG	GTG	GGG	GAG	GCA	ACT	GGT	GGT	CCT	GAG	576
V	P	R	G	E	S	E	E	T	G	S	S	E	G	A	P	S	1900
GTC	CCT	CGA	GGA	GAG	AGC	GAG	GAG	ACA	GGA	AGC	TCC	GAG	GGT	GCC	CCT	TCC	596
A	T	R	A	P	E	G	T	R	E	L	E	A	P	S	E	D	1960
GCC	ACA	CGG	GCC	CCT	GAG	GGT	ACC	AGG	GAG	CTG	GAG	GCC	CCC	TCT	GAA	GAT	616
																	2020

Fig. 24D

R T A P A G T S V Q A Q P V L P T D S A 636
 AGA ACT GCC CCA GCA GGG ACC TCA GTG CAG GCC CAG CCA GTG CTG CCC ACT GAC AGC GCC 2080

 S R G G V A V V P A S G N S A Q G S T A 656
 AGC CGA GGT GGA GTG GCC GTG GTC CCC GCA TCA GGT AAT TCT GCC CAA GGC TCA ACT GCC 2140

 L S I L L L F F P L Q L W V T * 672
 CTC TCT ATC CTA CTC CTT TTC TTC CCC CTG CAG CTC TGG GTC ACC TGA 2188

 CCTGTAGTCCTTTAAACCCACCATCATCCCAAACCTCCTGTCTTTGCCCTTCAATCTCTTACCCACCTCTACCTATGGG 2267

 TCTCCAATCTCGGATATCCACCTTGTGGGTATCTCAGCTCTCCGGTCTTTACCCGTGATCCAGCCCCGCCACTGAC 2346

 CATCTGTGACCCCTTCCCCTGCCATTGGGCCCCCTCCACCTGTGGCTCACATCTCGCCAGCCCCACAGAGCATCCTCAGGCCCT 2425
 CTCCAAGGGTCCTCATCACCTATTGCAGCCCTTCAGGGCTCGGCCCTATTTTCCACTACTCCCTTCATCCGCCCTGTGTGCC 2504

 GTCCCCCTTAGCTGCCCTCCTATTGATCTCAGGGAAGCCTGGGAGTCCCCTTCTCACCCCTCAACCTCCGGAGTCCAGGAG 2583

 AACCCGTACCCCCACAGAGCCTTAAGCAACTACTTCTGTGAAGTATTTTGTGACTGTTTTCATGGAAAACAAGCCTTGGA 2662

 AATAAATCTCTATTAAACCGCTTTGTAAACCAAAAAAATAAAAAAAGGGCGGCCGC 2730

Fig. 24E

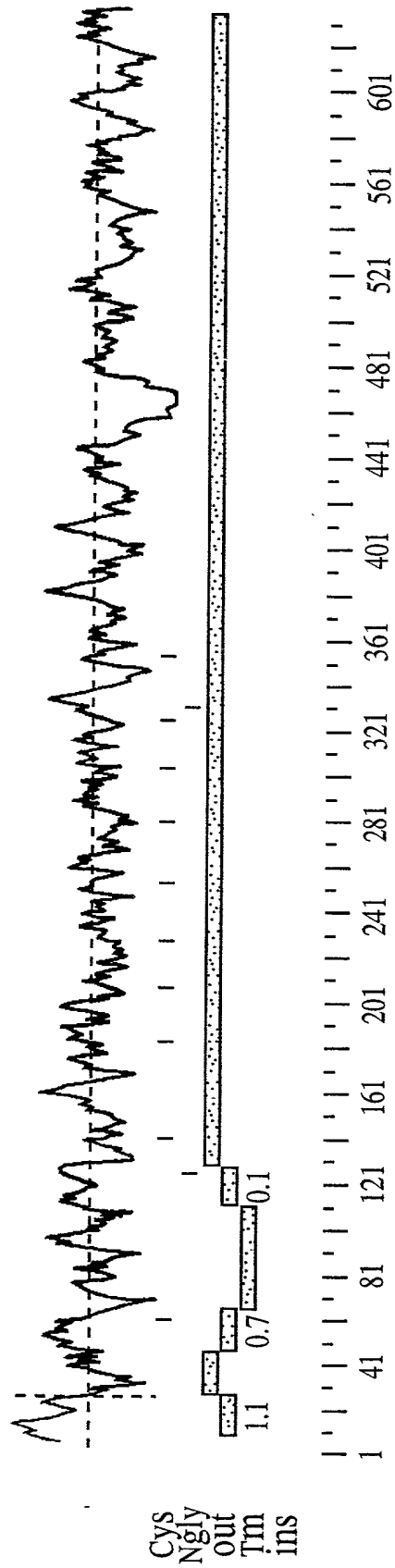


FIG. 24F

```

10      20      30      40      50      60      70
332 MAQLFLPLLAALVLAQAPAAALADVLEGDSSSEDRAFRVRIAGDAPLQGVLGALTIPCHVHYLRPPPSRRA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
BEF MAQLFLPLLAALVLAQAPAAALADVLEGDSSSEDRAFRVRIAGDAPLQGVLGALTIPCHVHYLRPPPSRRA
10      20      30      40      50      60      70

80      90      100     110     120     130     140
332 VLGSPRVKWTFLSRGREAEVLVARGVRVKVNEAYRFRVALPAYPASLTDVSLALSELRPNDSGIYRCEVQ
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
BEF VLGSPRVKWTFLSRGREAEVLVARGVRVKVNEAYRFRVALPAYPASLTDVSLALSELRPNDSGIYRCEVQ
80      90      100     110     120     130     140

150     160     170     180     190     200     210
332 HGIDSSDAVEVKVGCVFLYREGSARYAFSFGAQEACARIGAHIAATPEQLYAAAYLGGYEQCDAGWLSD
      ::::::::::::::
BEF HGIDSSDAVE-----SS
150

220     230     240     250     260     270     280
332 QTVRYPIQTPREACYGMDMGFPGRNYGVVDPDDLVDVYCYAEDLNGELFLGDPPEKLTLEEARAYCQER
      : ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
BEF Q--RYPIQTPREACYGMDMGFPGRNYGVVDPDDLVDVYCYAEDLNGELFLGDPPEKLTLEEARAYCQER
160     170     180     190     200     210     220

290     300     310     320     330     340     350
332 GAEIATTGQLYAAWDGGLDHCSPGWLADGSRYPYIVTPSQRCGGGLPGVKTLFLFPNQTFPKNKHSRFNV
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
BEF GAEIATTGQLYAAWDGGLDHCSPGWLADGSRYPYIVTPSQRCGGGLPGVKTLFLFPNQTFPKNKHSRFNV
230     240     250     260     270     280     290

```

Fig. 24G

Fig. 24H

Fig. 24H

Fig. 24I

```

350      360      370      380      390      400      410
M YCFRDSAHPSEASSPAS---DGLEAIVTVTEKLEELQLPQEAMESESRGAIYSIPISEDGGGSST
      :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
H YCFRDSAQPSAIPEASNPNASDPASDGLAIVTVTETLEELQLPQEATESESRGAIYSIPIMEDGGGSST
360      370      380      390      400      410      420

      420      430      440      450      460      470
M PEDPAEAPRTPLESETQSIAPPTESSEEEGVALEEEERFKDLEALEEKEQED----LWVWPRELSSP-
      :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
H PEDPAEAPRTLLLEFETQSMVPPTGFSEEEGKALEEEKEEEEEEEVEDEALWAWPSELSSPG
430      440      450      460      470      480      490

      480      490      500      510      520      530
M ----LPTGSET-EHSLSQVSPPAQAVLQLDASPSG-----PPRFRGPPAETLLPPREWS-ATSTPGG
      :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
H PEASLPTEPAAQEKSLSQ--APARAVLQPGASPLPDGESEASRPPRVHGPPTETLTPPRERNLASPSPT
500      510      520      530      540      550
      540      550      560      570      580      590      600
M ---AREVGGETGSPELSGVPR-ESEEAGSSSLEDGPSLLPATWAPVGPRELETPSEEKSGRTVLAGTSVQ
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
H LVEAREVGEATGGPELSGVPRGESEETGSS--EGAPSLLPATRAPEGTRELEAPSEDNSGRTAPAGTSVQ
560      570      580      590      600      610      620

      610      620      630      640      650      660      670
M AQPVLPTDSASHGGVAVAPSSGDCIPSPCHNGGTCLEEKEGFRCCLCPGYGGDLCDVGLHFCSPGWFAFQ
      ::::::::::::::::::::::: . :::::
H AQPVLPTDSASRGGVAVVPASGNSAQ-----GSTAL-----
630      640      650

```

Fig. 24J


```

680      690      700      710      720      730      740
M GACYKHFS TRRSWEAE SQCRALGAHLTS ICTPEEQDFVNDRYREYQWIGLNDRTIEGDFLWSDGAPLLY
H -----SI-----L-----LLF
      660

750      760      770      780      790      800      810
M ENWNPGQD SYFLSGENCVMVWHDQGWSDVPCNYHLSYTKMGLVSCGPPQLPLAQIFGRPRRLRYAV
H -----F-----PLQ-----
      :
      :
      :

820      830      840      850      860      870      880
M DTVLRYRCRDGLAQRNLP LIRCQENGLWEAPQISCVPRRPGRALRSMDAPEGPRGQLSRHRKAPLTTPSS
H -----LWVT-----
      670

```

M L

H -

Fig. 24K

Fig. 24L

```

340      350      360      370      380      390      400
H CATCCCTGCCACGTCCACTACCTGCGGCCACCGCCGAGCCGCCGGCTGTGCTGGCTCTCCGCGGTC
   :::::::::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
M CATCCCATGCCACGTCCACCACTGCGGCCCGCGCGCAGCCGCCGGCGCGGGTTTCCCGCGGTC
310      320      330      340      350      360      370

410      420      430      440      450      460      470
H AAGTGGACTTTCCTGTCCCGGGCGGGAGGCAGAGGTGCTGGTGCGCGGGGAGTGCGCGTCAAGGTGA
   :::::::::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
M AAGTGGACCTTCCCTGTCCGGGACCGGGAGGTAGAGGTTCTGGTGCTCGCGGGCTGCGCGTCAAGGTAA
380      390      400      410      420      430      440

480      490      500      510      520      530      540
H ACGAGGCCTACCGGTTCCCGGTGGCACTGCCCTGCGTACCCAGCGTCGCTCACCGACGTCTCCCTGGCGCT
   :::::::::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
M ACGAAGCCTACCGGTTCCCGGTGGCGCTGCCCTGCCCTACCCCGCATCGCTACGGATGTCTCTAGTATT
450      460      470      480      490      500      510

550      560      570      580      590      600      610
H GAGCGAGCTGCGCCCCAACGACTCAGGTATCTATCGCTGTGAGTCCAGCACGGCATCGATGACAGCAGC
   :::::::::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
M GAGCGAACTGCGGGCCCAATGATTCCGGGGTCTATCGCTGCGAGTCCAGCACGGTATCGACGACAGCAGT
520      530      540      550      560      570      580

620      630      640      650      660      670      680
H GACGCTGTGAGGTCAAGGTCAAAGGGTTCGTCTTCTCTACCGAGAGGGCTCTGCCCGCTATGCTTTCT
   :::::::::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
M GATGCTGTGAGGTCAAGGTCAAAGGGTTCGTCTTCTCTACAGAGAGGGCTCTGCGCGCTATGCTTTCT
590      600      610      620      630      640      650

```

Fig. 24M

```

690      700      710      720      730      740      750
H CCTTTCTGGGCCCCAGGAGGCCTGTGCCCCGCATTGGAGCCACATCGCCACCCCGGAGAGCTCTATGC
   ::::::::::::::::::::: : : : : : : : : : : : : : : : : : : : : : : : : : :
M CCTTCGCTGGAGCCCAGGAAGCCTGCGCTCGCATAGGAGCCCGAATCGCCACCCCGGAGAGCTCTATGC
660      670      680      690      700      710      720

760      770      780      790      800      810      820
H CGCCTACCTTGGGGCTATGAGCAATGTGATGCTGGCTGGCTGTCTGGATCAGACCGTGAGGTATCCCATC
   ::::::::::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M TGCCTACCTCGGCGGCTATGAGCAGTGTGATGCAGGCTGGCTGTCCGACCAAACCTGTGAGGTACCCCATC
730      740      750      760      770      780      790

830      840      850      860      870      880      890
H CAGACCCACGAGAGGCCTGTTACGGAGACATGGATGGCTTCCCCGGGTCCGGAACCTATGTTGGTGG
   ::::::::::::::::::::: : : : : : : : : : : : : : : : : : : : : : : : :
M CAGAACCCACGAGAGGCCTGCTCTGGAGACATGGATGGCTATCCTGGCTGCGGAACCTACGGAGTGGTGG
800      810      820      830      840      850      860

900      910      920      930      940      950      960
H ACCCGGATGACCTCTATGATGTGTACTGTATGCTGAAGACCTAAATGGAGAACTGTTCTGGGTGACCC
   . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M GTCCCTGATGATCTCTATGATGTCTACTGTATGCCGAAGACCTAAATGGAGAACTGTTCTAGGCGCCCC
870      880      890      900      910      920      930

970      980      990      1000      1010      1020      1030
H TCCAGAGAAGCTGACATTGGAGGAAGCACGGCGTACTGCCAGGAGCGGGTGCAGAGATTGCCACCACG
   :: .. ::::::::::::::: : : : : : : : : : : : : : : : : : : : : : : : :
M TCCCAGCAAGCTGACATGGGAGGAGGCTCGGGACTACTGTCTGGAACGTGTGTGCACAGATCGCTAGCACA
940      950      960      970      980      990      1000

```

Fig. 24N

Letter "Q" Refs

```

1040      1050      1060      1070      1080      1090      1100
H  GGCCAACTGTATGCAGCCTGGGATGGTGGCCCTGGACCACCTGCAGCCCCAGGTGGCTAGCTGATGGCAGTG
    ::::::::::::::::::::::::::: . ::::::::::: ::::::::::: ::::::::::: :
M  GGCCAGCTGTACGCAGCCTGGAATGGTGGCCCTGGACAGATGTAGCCCTGGCTGGCTGGCTGATGGCAGCG
1010      1020      1030      1040      1050      1060      1070

1110      1120      1130      1140      1150      1160      1170
H  TGCCTACCCCATCGTCACACCCAGCCAGCGCTGTGGTGGGGCTTGCCCTGGTGTCAAGACTCTCTTCCT
    ::::::::::: ::::::::::: ::::::::::: :: :: ::::::::::: ::::::::::: :::::::::::
M  TGCCTATCCCATCATCACACCCAGCCAAACGCTGTGGGGCGGCCCTGCCAGGAGTCAAGACCCTCTTTCCT
1080      1090      1100      1110      1120      1130      1140

1180      1190      1200      1210      1220      1230      1240
H  CTTCCCCAACCACTGGCTTCCCCAATAAGCACAGCCGCTTCAACGTCTACTGCTTCCGAGACTCGGCC
    :: ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::
M  CTTTCCCCAACCACTGGCTTCCCCCAGCAAGCAGAACCGCTTCAATGTCTACTGCTTCCGAGACTCTGCC
1150      1160      1170      1180      1190      1200      1210

1250      1260      1270      1280      1290      1300      1310
H  CAGCCTTCTGCCATCCCTGAGGCCCTCCAACCCAGCCTCCAACCCAGCCTCTGTATGGACTAGAGGCTATCG
    :: :: ::::: . : ::::::::::: ::::::::::: ::::::::::: . ::::::::::: :: ::
M  CATCCCTCTGCTTCTCTGAGGCCCTCTAGCCAGCCTC-----AGATGGACTTGAGGCCATTG
1220      1230      1240      1250      1260      1270

1320      1330      1340      1350      1360      1370      1380
H  TCACAGTGACAGAGACCCCTGGAGGAACTGCAGCTGCCTCAGGAAGCCACAGAGAGTGAATCCCCTGGGGC
    ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: :: :::::::::::
M  TCACAGTGACAGAAAAGCTGGAGGAACTGCAGCTGCCTCAGGAAGCGATGGAGAGCGAGTCTCGTGGGGC
1280      1290      1300      1310      1320      1330      1340

```

Fig. 240

Figure 24P

```

1390      1400      1410      1420      1430      1440      1450
H CATCTACTCCATCCCATCATGGAGGACGGAGGAGGTGGAAGCTCCACTCCAGAAAGACCCAGAGAGGCC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M CATCTACTCCATCCCATCATTCAGAAGATGGGGGAGGAGGAAGCTCCACCCAGAAAGACCCAGAGAGGCC
1350      1360      1370      1380      1390      1400      1410

1460      1470      1480      1490      1500      1510      1520
H CCTAGGACGCTCCTAGAAATTGAAACACAATCATGTACCGCCACGGGGTTCTCAGAAAGAGGAAGTA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M CCCAGGACTCCGCTAGAAATCGGAAACCAATCCATTGCACCACCTACCGAGTCCTCAGAAAGAGGAAGCGG
1420      1430      1440      1450      1460      1470      1480

1530      1540      1550      1560      1570      1580      1590
H AGGCATTGGAGGAAGAAGAGAAAATATGAAGATGAAGAAGAGAGGAGGAAGAAGAGAGGAGGT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M TAGCCCTGGAGGAAGAAGAAAGATTCAAAGAC-----TTGGAGGCTCTGGAGGAAGAGAAAGAGAGCA
1490      1500      1510      1520      1530      1540

1600      1610      1620      1630      1640      1650      1660
H GGAGGATGAGGCTCTGTGGGCATGGCCAGCGAGCTCAGCAGCCCGGGCCCTGAGGCCCTCTCTCCCCACT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M GGAGGA-----C-CTGTGGGTGTGGCCAGAGAGCTCAGCAGCCC-----TCTCCCTACT
1550      1560      1570      1580      1590

1670      1680      1690      1700      1710      1720
H GAGCCAGCAGCCAGGAGAAAGTCACTCTCCCAGG-----CGCCAGCAAGGGCAGTCTGCAGCCTGGTG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M GGCTCAGAAAC---AGAGCATTCACTCTCCCAGGTGTCCCCACCCAGCCAGGCAGTTCTACAGCTGGATG
1600      1610      1620      1630      1640      1650      1660

```

Fig. 24P

1730	1740	1750	1760	1770	1780	1790				
H	CATCACCAC	TTCTGTATG	GAGAGTCAG	AAGCTTCC	AGGCTTCC	AAGGTCATG	GACCACCTACT	GAGAC		
	:::::::::	:::::		:::::::::	:::::::::	:::::::::	:::::::::	:::::::::		
M	CGTCACCTT	CTCTCCTG	-----	GGCCTCCA	AGGTTCCG	TGGACCGC	CTGCAGAGAC			
1670			1680	1690	1700	1710				
1800	1810	1820	1830	1840	1850	1860				
H	TCTGCCAC	TCCAGGAG	AGGAACCT	AGCATCCC	ATCACCTT	CCACTCTG	GTGAGGCA	AGAGAGGTG		
	:::	:	:	:::::::::	:::	:::::	:::::	:::::::::		
M	TTTGCTCC	CCCCGAG	GGAGTGG	AGC-----	GCCACA	TCTACT-CC	-----	TGGT-GGGGCA	AGAGAA	GTA
1720	1730		1740	1750	1760	1770				
1870	1880	1890	1900	1910	1920	1930				
H	GGGAGGCA	ACTGGTGT	CTGAGCTAT	CTGGGGT	CCCCTCG	AGGAGAG	CGGAGAC	AGAGCTCC-		
	:::::::::	:::::	:	:::::::::	:::::	:::::	:::::	:::::::::		
M	GGGGGGA	AACTGG	AGCCCTG	AGCTCTCT	GGGTTCT	CTCGA--	-GAGAGC	GAGGAGGC	AGGAGCTCCA	
1780	1790	1800	1810	1820	1830					
1940	1950	1960	1970	1980	1990	2000				
H	-----	GAGGGT	GCCCCCTT	CCCCCTG	CTTCCAG	CCACACG	GGCCCCCTG	AGGTACC	AGGAGCTGG	AGGCCCC
	:::::::::	:::::::::	:::::::::	:::::	:::::	:::::	:::::	:::::	:::::::::	:::::::::
M	GCTTGAG	GATGCCCC	TTCCCTACT	TTCCAGCT	ATATGG	GGCCCCCTG	TGGTCCC	AGGAGCTG	GAGACCCC	
1840	1850	1860	1870	1880	1890	1900				
2010	2020	2030	2040	2050	2060	2070				
H	CTCTGA	AGATAATT	CTGGA	AGAACTG	CCCCAG	CAGGACCT	CAGTGC	AGGCCCC	AGCCAGTGT	GCCCCACT
	:::::::::	:::::	:::::::::	:::::	:::::	:::::	:::::	:::::	:::::::::	:::::::::
M	CTCAGA	AGAGAGT	CTGGA	AGAACTG	TCTTGG	CAGGCACCT	CAGTGC	AGGCCCC	AGCCAGTGT	GCCCCACC
1910	1920	1930	1940	1950	1960	1970				

Fig. 24Q

```

2080      2090      2100      2110      2120      2130
H  GACAGCGCCAGCGAGGTGGAGTGGCCGTGGTCCCCGCATCAGGTAATT-----CTGCCCAAGGCTCA
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  GACAGTGCCAGCACGCGTGGAGTGGCTGTGGCTCCCTCATCAGGTGACTGTATCCCCAGCCCTGCCACA
1980      1990      2000      2010      2020      2030      2040

H  A-----C-TGC-----2140      2150
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  ATGGTGGGACATGCTTGGAGGAGAAGGAGGGTTTCCGCTGCCTATGTTGCCAGGCTATGGGGGGGACCT
2050      2060      2070      2080      2090      2100      2110

2160      2170      2180      2190      2200
H  TTTC-----TTCCC--C---CTGCAGCTCTGG-----GTC--ACCTGA---CCTG---TAGTCCTTT
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  GTGCGATGTGGCCTTCATTCTGCAGCCCTGGCTGGGAGGCCCTTCCAGGGAGCCTGCTACAAGCACTTT
2120      2130      2140      2150      2160      2170      2180

H  AACCCAC-----2210      2220      2230
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  TCCACACGAAGGAGTTGGGAGGAGGCAGAAAGTCAAGTGCCGAGCGCTAGGTGCTCATCTGACCAAGCATCT
2190      2200      2210      2220      2230      2240      2250

H  GC-----CT-----2240      2250      2260      2270
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  GCACCCCTGAGGAGCAAGACTTTGTCAATGATCGATACCGGAGTACCAGTGAGTTGGGCTCAATGACAG
2260      2270      2280      2290      2300      2310      2320

```

Fig. 24R

Fig. 24S

Fig. 24S

```

2490      2500      2510      2520      2530
H CTTCA-TCCGCCCTGTGTGCC-----GTCC--CCTTTAGCTGC-CTCCT-----ATTGATCTC
: : : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M CCTCAGATTTCCTGTGTACCCCGGAGGCCCTGGCCGTGCTCTGCGCTCCATGGACGCCCCAGAGGACCAC
2680      2690      2700      2710      2720      2730      2740

2540
H AGGGA-AGC-----CTGGGAGTC-CC-TTCTCACC--CCTC-AACCTCCGGAGT-CCAGGAGAAC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M GGGACAGCTCTCGAGGCACAGGAAGCACCGTTGACACCGCCCTCCAGTCTCTAGGGAGCCTGGAAGAC
2750      2760      2770      2780      2790      2800      2810

2590      2600      2610      2620      2630
H CCGTACCCCCCA-CAGAGCCTTAA-GCAACTACT-----TCT-----GTGAAGTATTT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M TGCTGCCCCCAGCAGGACCCCTCTCACATCAACTGCCAGTGCTCTTCCCAATGATAGGGGTGACGTGAGA
2820      2830      2840      2850      2860      2870      2880

2640      2650
H ----TTTGACTGT--TTCA-----TGGAACA-----
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M GGGGTGGGACTGAAATTCAGAGGACAGCGCTCGAAGGGGTTTCTGGGAAACACTTGGGTGGCTCCGCCCC
2890      2900      2910      2920      2930      2940      2950

2660      2670      2680
H -----AGCCTTGGAAAT-----AAATCTCTATTAA-----AC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M CTCACACAAGGGCCTCAGGTTTACCCCGGTAAAGTCCCTAAGTGCCTCAACTGCCCTCTCATGTCAGCTGC
2960      2970      2980      2990      3000      3010      3020

```

Fig. 24T

Sequence

```

H CGCTTTGT-----AAC-----CAAAAAAAAAAAAAA      2690      2700
: : :::::      ::::      ::::      ::::      ::::      ::::
M CTCCTTGTCCTCGATNTCGTNAGGGGACACTGTGCTATTTCGATCTTGATTGTCGAAGAGTTTTTAGGAT
3030      3040      3050      3060      3070      3080      3090

2710
H AAA-----AAAAAAAAAGGGCGG--CC-----GC      2720      2730
:::      ::::      ::::      ::::      ::::      ::::      :
M GGAGTACCAGCAAAACCAGGTGGAATAAAGTTGTCTGAACCCCAAGAAAAA
3100      3110      3120      3130      3140      3150

```

Fig. 24U

Table 25A

M A P P A A R L A L L										11
GTCGACCCACGCTCCGCCACGCTCCGGCCC ATG GCG CCG CCC GCG GCG GCG CTC GCG CTC GCG CTC										66
S A A A L T L A A R P A P S P G L G P G										31
TCC GCC GCG GCG CTC ACG CTG GCG GCG CCC GCG CCT AGC CCC GCG CTC GCG CCC GCG GGA										126
P E C F T A A N G A D Y R G T Q N W T A L										51
CCC GAG TGT TTC ACA GCC AAT GGT GCG GAT TAT AGG GGA ACA CAG AAC TGG ACA GCA CTA										186
Q G G K P C L F W N E T F Q H P Y N T L										71
CAA GCG GGG AAG CCA TGT CTG TTT TGG AAC GAG ACT TTC CAG CAT CCA TAC AAC ACT CTG										246
K Y P N G E G G G GCG CTG GGT GAG CAC AAC TAT TGC AGA AAT CCA GAT GGA										91
AAA TAC CCC AAC GGG GAG GGG GCG CTG GGT GAG CAC AAC TAT TGC AGA AAT CCA GAT GGA										306
D V S P W C Y V A E H E D G V Y W K Y C										111
GAC GTG AGC CCC TGG TGC TAT GTG GCA GAG CAC GAG GAT GGT GTC TAC TGG AAG TAC TGT										366
E I P A C Q M P G N L G C Y K D H G N P										131
GAG ATA CCT GCT TGC CAG ATG CCT GGA AAC CTT GGC TGC TAC AAG GAT CAT GGA AAC CCA										426
P P L T G T S K T S N K L T I Q T C I S										151
CCT CCT CTA ACT GGC ACC AGT AAA ACG TCC AAC AAC AAA CTC ACC ATA CAA ACT TGC ATC AGT										486
F C R S Q R F K F A G M E S G Y A C F C										171
TTT TGT CGG AGT CAG AGG TTC AAG TTT GCT GGG ATG GAG TCA GGC TAT GCT TGC TTC TGT										546

Fig. 25A

G	N	N	P	D	Y	W	K	Y	G	E	A	A	S	T	E	C	N	S	V	191
GGA	AAC	AAT	CCT	GAT	TAC	TGG	AAG	TAC	GGG	GAG	GCA	GCC	AGT	ACC	GAA	TGC	AAC	AGC	GTC	606
C	F	G	D	H	T	Q	P	C	G	G	D	G	R	I	I	L	F	D	T	211
TGC	TTC	GGG	GAT	CAC	ACC	CAA	CCC	TGT	GGT	GGC	GAT	GGC	AGG	ATC	ATC	CTC	TTT	GAT	ACT	666
L	V	G	A	C	G	G	N	Y	S	A	M	S	S	V	V	Y	S	P	D	231
CTC	GTG	GGC	GCC	TGC	GGT	GGG	AAC	TAC	TCA	GCC	ATG	TCT	TCT	GTG	GTC	TAT	TCC	CCT	GAC	726
F	P	D	T	Y	A	T	G	R	V	C	Y	W	T	I	R	V	P	G	A	251
TTC	CCC	GAC	ACC	TAT	GCC	ACG	GGG	AGG	GTC	TGC	TAC	TGG	ACC	ATC	CGG	GTT	CCG	GGG	GCC	786
S	H	I	H	F	S	F	P	L	F	D	I	R	D	S	A	D	M	V	E	271
TCC	CAC	ATC	CAC	TTC	AGC	TTC	CCC	CTA	TTT	GAC	ATC	AGG	GAC	TCG	GCG	GAC	ATG	GTG	GAG	846
L	L	D	G	Y	T	H	R	V	L	A	R	F	H	G	R	S	R	P	P	291
CTT	CTG	GAT	GGC	TAC	ACC	CAC	CGT	GTC	CTA	GCC	CGC	TTC	CAC	GGG	AGG	AGC	CGC	CCA	CCT	906
L	S	F	N	V	S	L	D	F	V	I	L	Y	F	F	S	D	R	I	N	311
CTG	TCC	TTC	AAC	GTC	TCT	CTG	GAC	TTC	GTC	ATC	TTG	TAT	TTC	TTC	TCT	GAT	CGC	ATC	AAT	966
Q	A	Q	G	F	A	V	L	Y	Q	A	V	K	E	E	L	P	Q	E	R	331
CAG	GCC	CAG	GGA	TTT	GCT	GTT	TTA	TAC	CAA	GCC	GTC	AAG	GAA	GAA	CTG	CCA	CAG	GAG	AGG	1026

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Fig. 25B

Reference

P	A	V	N	Q	T	V	A	E	V	I	T	E	Q	A	N	L	S	V	S	351
CCC	GCT	GTC	AAC	CAG	ACG	GTG	GCC	GAG	GTG	ATC	ACG	GAG	CAG	GCC	AAC	CTC	AGT	GTC	AGC	1086
A	A	R	S	S	K	V	L	Y	V	I	T	T	S	P	S	H	P	P	Q	371
GCT	GCC	CGG	TCC	TCC	AAA	GTC	CTC	TAT	GTC	ATC	ACC	ACC	AGC	CCC	AGC	CAC	CCA	CCT	CAG	1146
T	V	P	G	S	N	S	W	A	P	P	M	G	A	G	S	H	R	V	E	391
ACT	GTC	CCA	GGT	AGC	AAT	TCC	TGG	GCG	CCA	CCC	ATG	GGG	GCT	GGA	AGC	CAC	AGA	GTT	GAA	1206
G	W	T	V	Y	G	L	A	T	L	L	I	L	T	V	T	A	I	V	A	411
GGA	TGG	ACA	GTC	TAT	GGT	CTG	GCA	ACT	CTC	CTC	ATC	CTC	ACA	GTC	ACA	GCC	ATT	GTA	GCA	1266
K	I	L	L	H	V	T	F	K	S	H	R	V	P	A	S	G	D	L	R	431
AAG	ATA	CTT	CTG	CAC	GTC	ACA	TTC	AAA	TCC	CAT	CGT	GTT	CCT	GCT	TCA	GGG	GAC	CTT	AGG	1326
D	C	H	Q	P	G	T	S	G	E	I	W	S	I	F	Y	K	P	S	T	451
GAT	TGT	CAT	CAA	CCA	GGG	ACT	TCG	GGG	GAA	ATC	TGG	AGC	ATT	TTT	TAC	AAG	CCT	TCC	ACT	1386
S	I	S	I	F	K	K	K	L	K	G	Q	S	Q	Q	D	D	R	N	P	471
TCA	ATT	TCC	ATC	TTT	AAG	AAG	AAA	CTC	AAG	GGT	CAG	AGT	CAA	CAA	GAT	GAC	CGC	AAT	CCC	1446
L	V	S	D	*																476
CTT	GTG	AGT	GAC	TAA																1461

Fig. 25C

AAACCCCACTGTGCCCTAGGACTTGAGGTCCCTCTTTGAGCTCAAGGCTGCCGTGGTCAACCTCTCCTGTGTTCTCTC 1540
 TGACAGACTCTTCCCTCCTCTCCCTCTGCTCGGCTCTTCCGCGAAACCTCTCCTCTACAGACTAGGAAGAGGCACCT 1620
 GCTGCCAGGGCAGGACAGCCTGGATTCTCTCTGCTT 1657

Fig. 25D

GTCGACCCACGGCTCCGCGCTCCCGGTGCTGCCCTCTGCCCCGGCGCGCGGGGTCCCCGCACTGACGGCC 79
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M A P A P A A R L A L L S A A A L T L A 19
 C ATG GCG CCG CCC GCC GCG CTC GCG CTG CTC TCC GCC GCT GCG CTC ACT CTG GCG 137

A R P A P G P R S G P E C F T A N G A D 39
 GCC CGG CCC GCG CCC GGT CCC CGC TCC GGC CCC GAG TGC TTC ACA GCC AAC GGT GCA GAT 197

Y R G T Q S W T A L Q G G GGT GGG AAG CCA TGT CTG TTC TGG AAC 257
 TAC AGG GGA ACA CAG AGC TGG ACA GCG CTG CAA GGT GGG AAG CCA TGT CTG TTC TGG AAC

E T F Q H P Y N T L K Y P N G E G L G 79
 GAG ACT TTC CAG CAT CCG TAC AAC ACG CTG AAG TAC CCC AAC GGG GAA GGA CTG GGC 317

E H N Y C R N P D G D V S P W C Y V A E 99
 GAG CAC AAT TAT TGC AGA AAT CCA GAT GGA GAC GTG AGC CCT TGG TGC TAC GTG GCC GAG 377

Fig. 25E

H E D G V Y W K Y C E I P A C Q M P G N 119
CAT GAG GAC GGA GTC TAC TGG AAG TAC TGT GAA ATT CCT GCC TGC CAG ATG CCT GGA AAC 437

L G C Y K D H G N P P P L T G T S K T S 139
CTT GGC TGC TAC AAG GAT CAT GGA AAC CCA CCT CCT CTC ACG GGC ACC AGT AAA ACC TCT 497

N K L T I Q T C I S F C R S Q R F K F A 159
AAC AAG CTC ACC ATA CAA ACC TGT ATC AGC TTC TGT CGG AGT CAG AGA TTC AAG TTT GCT 557

G M E S G Y A C F C G N N P D Y W K H G 179
GGG ATG GAG TCA GGC TAT GCC TGC TTC TGT GGG AAC AAT CCT GAC TAC TGG AAG CAC GGG 617

E A A S T E C N S V C F G D H T Q P C G 199
GAG GCG GCC AGC ACC GAG TGC AAT AGT GTC TGC TTC TGC GGG GAC CAC ACG CAG CCC TGC GGT 677

G D G R I I L F D T L V G A C G G N Y S 219
GGG GAC GGC AGG ATT ATC CTC TTT GAC ACT CTC GTG GGC GCC TGC GGT GGG AAC TAC TCA 737

A M A A V V Y S P D F P D T Y A T G R V 239
GCC ATG GCA GCC GTG GTG TAC TCC CCT GAC TTC CCT GAC ACC TAC GCC ACT GGC AGA GTC 797

C Y W T I R V P G A S R I H F N F T L F 259
TGC TAC TGG ACC ATC CGG GTT CCA GGA GCC TCT CGC ATC CAT TTC AAC TTC ACC CTG TTT 857

D I R D S A D M V E L L D G Y T H R V L 279
GAT ATC AGG GAC TCT GCA GAC ATG GTG GAG CTG CTG GAC GGC TAC ACC CAC CGC GTC CTG 917

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Fig. 25F

V	R	L	S	G	R	S	R	P	P	L	S	F	N	V	S	L	D	F	V	299
GTC	CGG	CTC	AGT	GGG	AGG	AGC	CGC	CCG	CCT	CTG	TCT	TTC	AAT	GTC	TCT	CTG	GAT	TTT	GTC	977
I	L	Y	F	F	S	D	R	I	N	Q	A	Q	G	F	A	V	L	Y	Q	319
ATT	TTG	TAT	TTC	TTC	TCT	GAT	CGC	ATC	AAT	CAG	GCC	CAG	GGA	TTT	GCT	GTG	TTG	TAC	CAA	1037
A	T	K	E	E	P	P	Q	E	R	P	A	V	N	Q	T	L	A	E	V	339
GCC	ACC	AAG	GAG	GAA	CCG	CCA	CAG	GAG	AGA	CCT	GCT	GTC	AAC	CAG	ACC	CTG	GCA	GAG	GTG	1097
I	T	E	Q	A	N	L	S	V	S	A	A	H	S	S	K	V	L	Y	V	359
ATC	ACC	GAG	CAA	GCC	AAC	CTC	AGT	GTC	AGC	GCT	GCC	CAC	TCC	TCC	AAA	GTC	CTC	TAT	GTC	1157
I	T	P	S	P	S	H	P	P	Q	T	A	Q	V	A	I	P	G	H	R	379
ATC	ACC	CCC	AGC	CCC	AGC	CAC	CCT	CCG	CAG	ACT	GCC	CAG	GTA	GCC	ATT	CCT	GGG	CAC	CGT	1217
Q	L	G	P	T	A	T	E	W	K	D	G	L	C	T	A	W	R	P	S	399
CAG	TTG	GGG	CCA	ACA	GCC	ACA	GAG	TGG	AAG	GAT	GGA	CTG	TGT	ACG	GCC	TGG	CGA	CCC	TCC	1277
S	S	S	Q	S	Q	Q	L	S	Q	R	F	F	C	M	S	H	L	N	L	419
TCA	TCC	TCA	CAG	TCA	CAG	CAG	TTG	TCG	CAA	AGA	TTC	TTC	TGC	ATG	TCA	CAT	TTA	AAT	CTC	1337
I	E	S	L	H	Q	E	T	L	G	T	V	V	S	L	G	L	L	E	I	439
ATC	GAG	TCC	CTG	CAT	CAG	GAG	ACC	TTA	GGG	ACT	GTC	GTC	AGC	CTG	GGG	CTT	CTG	GAG	ATA	1397
S	G	P	F	S	M	N	L	P	L	Q	S	P	S	L	R	R	S	S	R	459
TCT	GGA	CCA	TTT	TCT	ATG	AAC	CTT	CCA	CTA	CAA	TCT	CCA	TCT	TTA	AGA	AGA	AGC	TCA	AGG	1457

Fig. 25G

V R V N K M T A I P S *
GTC AGA GTC AAC AAG ATG ACC GCA ATC CCC TCG TGA 471
1493
GTGACTGAAGCCACGCTGCATGAGAGGCTCCGCTCCAAGCTCGAGTTTGCTCCCTGAGTTCTCCTCTGATGAGTTC 1572
CCTGCCCTCCCATTCACCAACATCTCTTTTGGAGCACCTGCTTTAGAGGCAGCCAGCTGGGATCCTCCATCACAT 1651
GTACCAGCCTGGCTGCTCTGCTGGGATGGTAAGACAGGCCAGGCTGACGACACAGCTGGACCTGACTCCAGAAGA 1730
CTCTTGGTGGTGGGAGGTATAGTGAAGATGAGTTTCTTGTCTTCTCTGTTTGTCCACATACAGATCGGTTTC 1809
CCCTGTCTTTACAGTTTGCAATAGAGCCAGACTGAAAGAACTGTCAAGTTTCTAGGCTGGCTGGTTCCCCACTAAGA 1888
GTGGCATTTGGCCCCAGAGGCCAGAGGCCAGTGTAGGCTTTTCTGCTGCCAACTACCATGTGTCACT 1967
AGTCCAGGGGACTGAGAGCAGGGCCACACCATGTCATCTTTCTAGAGGTTCTTTTAGTACCCACTGACCAATGG 2046
GGCAAGCCTGAGGATTGGTCCATCTGTGTGGAATCAGAAATTCAGCCTGTCTTCTGCTCAGCCCCAAGCCTGTAGCCTAG 2125
TAGCCCTCAAGTAGTTGCCAATCCTGTGGAAATCAGAAATTCAGCCTGTCTTCTGCTCAGCCCCAAGCCTGTAGCCTAG 2204
AGCTGGGCTGTAGCCTAGAGCTGGGCTGTAGCCTAGAGCTGGGCTGTAGCACAGAGCTGGGCTGTAGCCTAGAGC 2283
TGGGCTGTAGCACAGAGCTGGGCTGTAGCCTAGAGCTGGGCTGTAGCACAGAGCTGGGCTGTAGCACAGAGCTGG 2362
GGCTGTAGCCTAGAGCTGGGCTGTAGCACAGAGCTGGGCTGTAACTCAGCGATCAAGAGCTTGCTTTGTATACATCG 2441
GACCCTAGGTTCTATCCCAGCACTATCAGAAGGTGGAGAGAAAAGACTGCACCATAGCATCGGGCAGCATCTGTGG 2520
TTCCTACGTGAGGTGCATCATTTTAAAGCAGATCAAACCTACCGGAGTTTGTCTTGTCCCTTATCATGGGAGC 2599
AGAGTAGGAGTAAGGGCTCTGGTCTTGCTCATTTGCTCCAGACAGGGAGGCAAAAGGTCAGGCTTGGAAGCTGGA 2678
GATCCTCCAGGAAAAGCTGCAAGATTGAGAGACCCAGCTGCAGTTGGGAGAGGAGGCCATCCCGACTGAGAAGTC 2757
CTGCAGTCTGGAAGTGCCCTTTGTAGCAGCAGCTGTGCCCTGAAGGTAGACCTTGGTCACCTCTCCTGCCAGCCCTGA 2836
GCCCTGCTCTCCTGGGTACCCCTCCTGGAACACCATGCTAACCTTCCCCGAGTCTCTCAGTCACTGCCATTGAGGCCCTC 2915
TCCCTAGCTGCTGCCAGGACTGTCTGGGGCCATCTGGGGATCAGGGAGAGGCAGCAGGAGTACTGACGAGGCAG 2994
TGACCTGAGCTGATGATCAACAGAGGACACAGAGTCTACAGTGGCTGGCTGCTGCTCAGCTCCTATGGGAGGCC 3073
TACAGGGGTACTAAGCTAGGGGTCTCATCTCATTTGATCTGGGAAAGGCTACAGGCTCCTGGATGTGAAGACAGGCC 3152
CACTACATAAGAACCACTGGAAATAGACTGACAGGAGCAGGTTCCACTCTAGGCTGTCCATAGCGTTTGCAGGACTC 3231

Fig. 25H

CCCTGAGACCAAGTTGAGTCACAGAGTGCCATGTGCGTAGTGCAATAAGGATATGGGTTCTTAACCAGGGAAGGCTC 3310
 ATAGCAGGCCAGGACATTTTTCAGCTCAGAGCACTGGCCCCAGGCTTCCTCTAAGCCACCACTCACCTGTCTCTCCT 3389
 ATCTCGACACAGGAAGCAAGCCCCAGTGTGTGGCAGCTGCGGCTCAGCATTTGGTGTCCCCAGGAAGGCGGTGGATG 3468
 TGGCCACGCTCCTTTTGTGTGGCCTGGCACAGCCCCAACACTGCAGGGCCCACCTTCTCTTTGGGGGTAGGGACAC 3547
 ATAAGGAAAACATAACCCACCTCCAAACACAGCAGAGGACAGTGGGAAGGAGGCTGTAAATCACCCAGGCCAGACCTC 3626
 CAGAAATGACAGGCACAGTCTGTAGAACCTGTAGGCAGCCAGTCAAGAGGGCTTTGTGCTGGTAACACCCCTGCCCTG 3705
 GAGCATAGGGGTAAGCCGAGGAGAGAGCAGCCCTCAGAGACATCAGCTAAAACATAGGTGCCCTATGTCCCTCCCT 3784
 TCCTGTCACACTGCTTACAAAGCAGACAGAGTAGGAAAGAGGTCTTCATCCTCTCCACATCAGCAAGGATAGGGCT 3863
 GCGGCTGCCATAAGTGAGCAAGGAGAACAGAGCTCTGGACTTCTCTAAATGTGGGCTCTGGCTTCAGACTCCTCAGCCA 3942
 AAAGCTCTTGAAGATCAAAGCTCTGGCGGTACAGCTGTCCCTGTGGCCAGCCCATGGGATGTGCCCTGGGCCAG 4021
 GTGCCACCCACGGCTCACTGTCAATCCAGGAGGACCCCACTGATGCTCTCATCATCCGCTGGCCTGACACTATCA 4100
 GAGCTCGCGCCGCTGTTGCCAGGCAGACTGACTACACTTGACCTTCAAGAGCACTTAGAAGTGGATGGCCTCCAGA 4179
 CTCGTGTCAGCCTCTGCAGGGCCACACAAGTCTCCGAGCCCAAGTCCACAAGCCTCCATGGTTCCCTGGCTCCTCCT 4258
 GTGGAGTGCTCCTGTTGATGCTGAGGTCTGCTTTGGGTACCGCCCTGGGAACCTGCTAACCTCCGATGGTCCCTTGT 4337
 GTCCTGTTTACTGCTCTTCTACCTCCAGGTCACTTAGCTCTGGCTGCTCTGGAGTGGGGGTGGGATGCT 4416
 GGGTGCAACCCCACTGGTCTGCCAACAGAACCTGGGGGCTCACACGGGCTCCTGTCTTGCCAAAGCTGGAGCTGAGC 4495
 AACTGGCCAGGCTGAGTGGGCAGAGCAAAACAAGTGAAGGGATCTCTCTCCTTAGAGGGAGGTGGCCGAAGGTGT 4574
 AGATCCAGCGAGGAGCTGCCATCCCCGCCACCTTCATAGCAGCAAGACCTTCCCATTTCCAAATCTCACCCCTCCAGCAG 4653
 GGATATGACTTTGGACAACAAGGCTTTATTTGTAATAATGCTCTTAATATGCAACTTTGAGAAATAAGATAGAAACATCA 4732
 TGTATTTTAAATAATAAATGAAGTGTGACACACTGTATACAATTTAAATATATATTTTAGGATTTTGTATTAAAGAA 4811
 AATGGAATGTGATGGTAACTTTTACAAAAGAGAGAAAAATGTTATTTTACTGTTTGAAGAAAAATAATATTTCTCA 4890
 TTGTTGTAGAAAAAATAAAAAAAGGGCGGCCG 4928

Fig. 25I

Fig. 25J

Fig. 25K

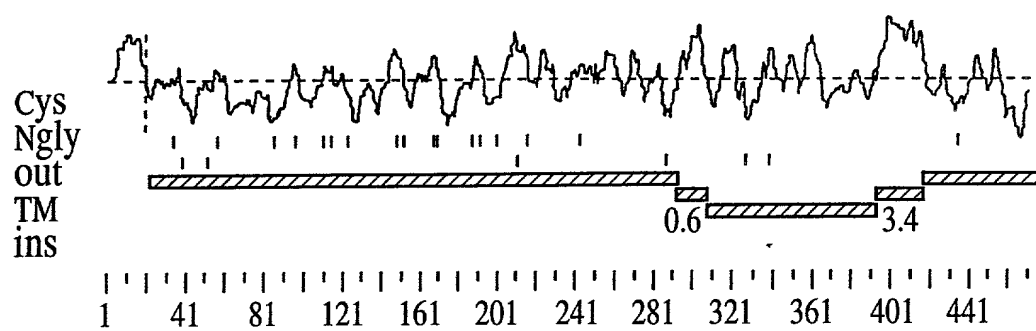


Fig. 25L

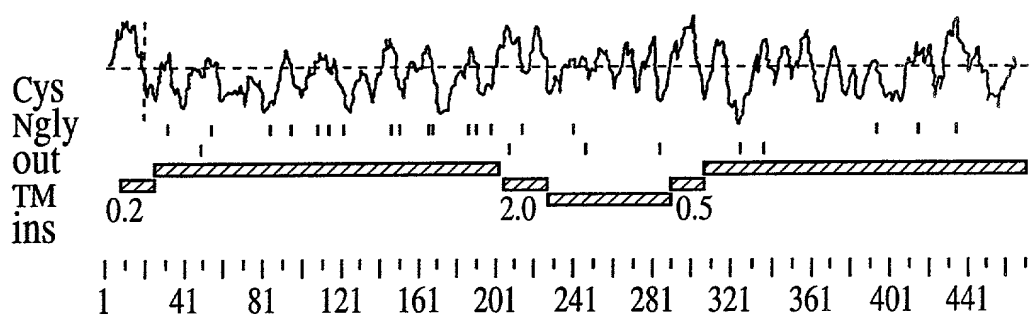


Fig. 25M

M M L P Q N S W H I D F G																13
GCGGCCGCTCGCGATCTAGAACTAGTA ATG ATG CTG CCT CAA AAC TCG TGG CAT ATT GAT TTT GGA																66
R C C C H Q N L F S A V V T C I L L N																33
AGA TGC TGC TGT CAT CAG AAC CTT TTC TCT GCT GTG GTA ACT TGC ATC CTG CTC CTG AAT																126
S C F L I S S F N G T D L E L R L V N G																53
TCC TGC TTT CTC ATC AGC AGT TTT AAT GGA ACA GAT TTG GAG TTG AGG CTG GTC AAT GGA																186
D G P C S G T V E V K F Q G W G T V C																73
GAC GGT CCC TGC TCT GGG ACA GTG GAG GTG AAA TTC CAG GGA CAG TGG GGG ACT GTG TGT																246
D D G W N T T A S T V V C K Q L G C P F																93
GAT GAT GGG TGG AAC ACT ACT GCC TCA ACT GTC GTG TGC AAA CAG CTT GGA TGT CCA TTT																306
S F A M F R F G Q A V T R H G K I W L D																113
TCT TTC GCC ATG TTT CGT TTT GGA CAA GCC GTG ACT AGA CAT GGA AAA ATT TGG CTT GAT																366
D V S C Y G N E S A L W E C Q H R E W G																133
GAT GTT TCC TGT TAT GGA AAT GAG TCA GCT CTC TGG GAA TGT CAA CAC CGG GAA TGG GGA																426
S H N C Y H G E D V G V N C Y G E A N L																153
AGC CAT AAC TGT TAT CAT GGA GAA GAT GTT GGT GTG AAC TGT TAT GGT GAA GCC AAT CTG																486

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Fig. 26A

G L R L V D G N N S C S G R V E V K F Q 173
 GGT TTG AGG CTA GTG GAT GGA AAC AAC TCC TGT TCA GGG AGA GTG GAG GTG AAA TTC CAA 546

 E R W G T I C D D G W N L N T A A V V C 193
 GAA AGG TGG GGG ACT ATA TGT GAT GAT GGG TGG AAC TTG AAT ACT GCT GCC GTG GTG TGC 606

 R Q L G C P S S F I S S G V V N S P A V 213
 AGG CAA CTA GGA TGT CCA TCT TCT TCT ATT TCT TCT GGA GTT GTT AAT AGC CCT GCT GTA 666

 L R P I W L D D I L C Q G N E L A L W N 233
 TTG CGC CCC ATT TGG CTG GAT GAC ATT TTA TGC CAG GGG AAT GAG TTG GCA CTC TGG AAT 726

 C R H R G W G N H D C S H N E D V T L T 253
 TGC AGA CAT CGT GGA TGG GGA AAT CAT GAC TGC TGC AGT CAC AAT GAG GAT GTC ACA TTA ACT 786

 C Y D S S D L E L R L V G G T G G A C T T G T A G G T G G A C T A A C C G C T G T A T G G G 846
 TGT TAT GAT AGT AGT GAT CTT GAA CTA AGG CTT GTA GGT GGA ACT AAC AAC CGC TGT ATG GGG

 R V E L K I Q G R W G T V C H H K W N N 293
 AGA GTA GAG CTG AAA ATC CAA GGA AGG TGG GGG ACC GTA TGC TGC CAC CAT CAT AAG TGG AAC AAT 906

 A A A D V V C K Q L G C G T A L H F A G 313
 GCT GCA GCT GAT GTC GTA TGC AAG CAG TTG GGA TGT GGA ACC GCA CTT CAC TTC GCT GGC 966

 L P H L Q S G S D V V W L D G V S C S G 333
 TTG CCT CAT TTG CAG TCA GGG TCT GAT GTT GTA TGG CTT GAT GGT GTC TCC TGC TCC GGT 1026

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Fig. 26B

N	E	S	F	L	W	D	C	R	H	S	G	T	V	N	F	D	C	L	H	353
AAT	GAA	TCT	TTT	CTT	TGG	GAC	TGC	AGA	CAT	TCC	GGA	ACC	GTC	AAT	TTT	GAC	TGT	CTT	CAT	1086
Q	N	D	V	S	V	I	C	S	D	G	A	D	L	E	L	R	L	A	D	373
CAA	AAC	GAT	GTG	TCT	GTG	ATC	TGC	TCA	GAT	GGA	GCA	GAT	TTG	GAA	CTG	CGA	CTA	GCA	GAT	1146
G	S	N	N	C	S	G	R	V	E	V	R	I	H	E	Q	W	T	I	393	
GGA	AGT	AAC	AAT	TGT	TCA	GGG	AGA	GTA	GAG	GTG	AGA	ATT	CAT	GAA	CAG	TGG	TGG	ACA	ATA	1206
C	D	Q	N	W	K	N	E	Q	A	L	V	V	C	K	Q	L	G	C	P	413
TGT	GAC	CAG	AAC	TGG	AAG	AAT	GAA	CAA	GCC	CTT	GTG	GTT	TGT	AAG	CAG	CTA	GGA	TGT	CCG	1266
F	S	V	F	G	S	R	R	A	K	P	S	N	E	A	R	D	I	W	I	433
TTC	AGC	GTC	TTT	GGC	AGT	CGT	CGT	GCT	AAA	CCT	AGT	AAT	GAA	GCT	AGA	GAC	ATT	TGG	ATA	1326
N	S	I	S	C	T	G	N	E	S	A	L	W	D	C	T	Y	D	G	K	453
AAC	AGC	ATA	TCT	TGC	ACT	GGG	AAT	GAG	TCA	GCT	CTC	TGG	GAC	TGC	ACA	TAT	GAT	GGA	AAA	1386
A	K	R	T	C	F	R	R	S	D	A	G	V	I	C	S	D	K	A	D	473
GCA	AAG	CGA	ACA	TGC	TTC	CGA	AGA	TCA	GAT	GCT	GGA	GTA	ATT	TGT	TCT	GAT	AAG	GCA	GAT	1446
L	D	L	R	L	V	G	A	H	S	P	C	Y	G	R	L	E	V	K	Y	493
CTG	GAC	CTA	AGG	CTT	GTC	GGG	GCT	CAT	AGC	CCC	TGT	TAT	GGG	AGA	TTG	GAG	GTG	AAA	TAC	1506
Q	G	E	W	G	T	V	C	H	D	R	W	S	T	R	N	A	A	V	V	513
CAA	GGA	GAG	TGG	GGG	ACT	GTG	TGT	CAT	GAC	AGA	TGG	AGC	ACA	AGG	AAT	GCA	GCT	GTT	GTG	1566

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Fig. 26C

C K Q L G C G K P M H V F G M T Y F K E 533
TGT AAA CAA TTG GGA TGT GGA AAG CCT ATG CAT GTG TTT GGT ATG ACC TAT TTT AAA GAA 1626

A S G P I W L D D V S C I G N E S N I W 553
GCA TCA GGA CCT ATT TGG CTG GAT GAC GTT TCT TGC ATT GGA AAT GAG TCA AAT ATC TGG 1686

D C E H S G W G K H N C V H R E D V I V 573
GAC TGT GAA CAC AGT GGA TGG GGA AAG CAT AAT TGT GTA CAC AGA GAG GAT GTG ATT GTA 1746

T C S G D A T W G L R L V G G S N R C S 593
ACC TGC TCA GGT GAT GCA ACA TGG GGC CTG AGG CTG GTG GGC GGC AGC AAC CGC TGC TCG 1806

G R L E V Y F Q G R W G T V C D D G W N 613
GGA AGA CTG GAG GTG TAC TTT CAA GGA CGG TGG GGC ACA GTG TGT GAT GAC GGC TGG AAC 1866

S K A A A V V C S Q L D C P S S I I G M 633
AGT AAA GCT GCA GCT GTG GTG TGT AGC CAG CTG GAC TGC CCA TCT TCT ATC ATT GGC ATG 1926

G L G N A S T G Y G K I W L D D V S C D 653
GGT CTG GGA AAC GCT TCT ACA GGA TAT GGA AAA ATT TGG CTC GAT GAT GTT TCC TGT GAT 1986

G D E S D L W S C R N S G W G N N D C S 673
GGA GAT GAG TCA GAT CTC TGG TCA TGC AGG AAC AGT GGG TGG GGA AAT AAT GAC TGC AGT 2046

H S E D V G V I C S D A S D M E L R L V 693
CAC AGT GAA GAT GTT GGA GTG ATC TGT TCT GAT GCA TCG GAT ATG GAG CTG AGG CTT GTG 2106

Fig. 26D

G	G	S	S	R	C	A	G	K	V	E	V	N	V	Q	G	A	V	G	I	713
GGT	GGA	AGC	AGC	AGG	TGT	GCT	GGA	AAA	GTT	GAG	GTG	AAT	GTC	CAG	GGT	GCC	GTG	GGA	ATT	2166
L	C	A	N	G	W	G	M	N	I	A	E	V	V	C	R	Q	L	E	C	733
CTG	TGT	GCT	AAT	GGC	TGG	GGA	ATG	AAC	ATT	GCT	GAA	GTT	GTT	TGC	AGG	CAA	CTT	GAA	TGT	2226
G	S	A	I	R	V	S	R	E	P	H	F	T	E	R	T	L	H	I	L	753
GGG	TCT	GCA	ATC	AGG	GTC	TCC	AGA	GAG	CCT	CAT	TTC	ACA	GAA	AGA	ACA	TTA	CAC	ATC	TTA	2286
M	S	N	S	G	C	T	G	G	E	A	S	L	W	D	C	I	R	W	E	773
ATG	TCG	AAT	TCT	GGC	TGC	ACT	GGA	GGG	GAA	GCC	TCT	CTC	TGG	GAT	TGT	ATA	CGA	TGG	GAG	2346
W	K	Q	T	A	C	H	L	N	M	E	A	S	L	I	C	S	A	H	R	793
TGG	AAA	CAG	ACT	GCG	TGT	CAT	TTA	AAT	ATG	GAA	GCA	AGT	TTG	ATC	TGC	TCA	GCC	CAC	AGG	2406
Q	P	R	L	V	G	A	D	M	P	C	S	G	R	V	E	V	K	H	A	813
CAG	CCC	AGG	CTG	GTT	GGA	GCT	GAT	ATG	CCC	TGC	TCT	GGA	CGT	GTT	GAA	GTG	AAA	CAT	GCA	2466
D	T	W	R	S	V	C	D	S	D	F	S	L	H	A	A	N	V	L	C	833
GAC	ACA	TGG	CGC	TCT	GTC	TGT	GAT	TCT	GAT	TTC	TCT	CTT	CAT	GCT	GCC	AAT	GTG	CTG	TGC	2526
R	E	L	N	C	G	D	A	I	S	L	S	V	G	D	H	F	G	K	G	853
AGA	GAA	TTA	AAT	TGT	GGA	GAT	GCC	ATA	TCT	CTT	TCT	GTG	GGA	GAT	CAC	TTT	GGA	AAA	GGG	2586
N	G	L	T	W	A	E	K	F	Q	C	E	G	S	E	T	H	L	A	L	873
AAT	GGT	CTA	ACT	TGG	GCC	GAA	AAG	TTC	CAG	TGT	GAA	GGG	AGT	GAA	ACT	CAC	CTT	GCA	TTA	2646

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Fig. 26E

C P I V Q H P E D T C I H S R E V G V 893
TGC CCC ATT GTT CAA CAT CCG GAA GAC ACT TGT ATC CAC AGC AGA GAA GTT GGA GTT GTC 2706

C S R Y T D V R L V N G K S Q C D G Q V 913
TGT TCC CGA TAT ACA GAT GTC CGA CTT GTG AAT GGC AAA TCC CAG TGT GAC GGG CAA GTG 2766

E I N V L G H W G S L C D T H W D P E D 933
GAG ATC AAC GTG CTT GGA CAC TGG GGC TCA CTG TGT GAC ACC CAC TGG GAC CCA GAA GAT 2826

A R V L C R Q L S C G T A L S T T G G K 953
GCC CGT GTT CTA TGC AGA CAG CTC AGC TGT GGG ACT GCT CTC TCA ACC ACA GGA GGA AAA 2886

Y I G E R S V R V W G H R F H C L G N E 973
TAT ATT GGA GAA AGA AGT GTT CGT GTG TGG GGA CAC AGG TTT CAT TGC TTA GGG AAT GAG 2946

S L L D N C Q M T V L G A P P C I H G N 993
TCA CTT CTG GAT AAC TGT CAA ATG ACA GGA AGC CTT GGA GCA CCT CCC TGT ATC CAT GGA AAT 3006

T V S V I C T G S L T Q P L F P C L A N 1013
ACT GTC TCT GTG ATC TGC ACA GGA AGC CTG ACC CAG CCA CTG TTT CCA TGC CTC GCA AAT 3066

V S D P Y L S A V P E G S A L I C L E D 1033
GTA TCT GAC CCA TAT TTG TCT GCA GTT CCA GAG GGC AGT GCT TTG ATC TGC TTA GAG GAC 3126

K R L R L V D G D S R C A G R V E I Y H 1053
AAA CGG CTC CGC CTA GTG GAT GGG GAC AGC CGC TGT GCC GGG AGA GTA GAG ATC TAT CAC 3186

Fig. 26F

D	G	F	W	G	T	I	C	D	D	G	W	D	L	S	D	A	H	V	V	1073
GAC	GGC	TTC	TGG	GGC	ACC	ATC	TGT	GAT	GAC	GAC	TGG	GAC	CTG	AGC	GAT	GCC	CAC	GTG	GTG	3246
C	Q	K	L	G	C	G	V	A	F	N	A	T	V	S	A	H	F	G	E	1093
TGT	CAA	AAG	CTG	GGC	TGT	GGA	GTG	GCC	TTC	AAT	GCC	ACG	GTC	TCT	GCT	CAC	TTT	GGG	GAG	3306
G	S	G	P	I	W	L	D	D	L	N	C	T	G	T	E	S	H	L	W	1113
GGG	TCA	GGG	CCC	ATC	TGG	CTG	GAT	GAC	CTG	AAC	TGC	ACA	GGA	ACG	GAG	TCC	CAC	TTG	TGG	3366
Q	C	P	S	R	G	W	G	Q	H	D	C	R	H	K	E	D	A	G	V	1133
CAG	TGC	CCT	TCC	CGC	GGC	TGG	GGG	CAG	CAC	GAC	TGC	AGG	CAC	AAG	GAG	GAC	GCA	GGG	GTC	3426
I	C	S	E	F	T	A	L	R	L	Y	S	E	T	E	T	E	S	C	A	1153
ATC	TGC	TCA	GAA	TTC	ACA	GCC	TTG	AGG	CTC	TAC	AGT	GAA	ACT	GAA	ACA	GAG	AGC	TGT	GCT	3486
289/361																				
G	R	L	E	V	F	Y	N	G	T	W	G	S	V	G	R	R	N	I	T	1173
GGG	AGA	TTG	GAA	GTC	TTC	TAT	AAC	GGG	ACC	TGG	GGC	AGC	GTC	GGC	AGG	AGG	AAC	ATC	ACC	3546
T	A	I	A	G	I	V	C	R	Q	L	G	C	G	E	N	G	V	V	S	1193
ACA	GCC	ATA	GCA	GGC	ATT	GTG	TGC	AGG	CAG	CTG	GGC	TGT	GGG	GAG	AAT	GGA	GTT	GTC	AGC	3606
L	A	P	L	S	K	T	G	S	G	F	M	W	V	D	D	I	Q	C	P	1213
CTC	GCC	CCT	TTA	TCT	AAG	ACA	GGC	TCT	GGT	TTC	ATG	TGG	GTG	GAT	GAC	ATT	CAG	TGT	CCT	3666
K	T	H	I	S	I	W	Q	C	L	S	A	P	W	E	R	R	I	S	S	1233
AAA	ACG	CAT	ATC	TCC	ATA	TGG	CAG	TGC	CTG	TCT	GCC	CCA	TGG	GAG	CGA	AGA	ATC	TCC	AGC	3726

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Fig. 26G

P	A	E	E	T	W	I	T	C	E	D	R	I	R	V	R	G	G	D	T	1253
CCA	GCA	GAA	GAG	ACC	TGG	ATC	ACA	TGT	GAA	GAT	AGA	ATA	AGA	GTG	CGT	GGA	GGA	GAC	ACC	3786
E	C	S	G	R	V	E	I	W	H	A	G	S	W	G	T	V	C	D	D	1273
GAG	TGC	TCT	GGG	AGA	GTG	GAG	ATC	TGG	CAC	GCA	GGC	TCC	TGG	GGC	ACA	GTG	TGT	GAT	GAC	3846
S	W	D	L	A	E	A	E	V	V	C	Q	Q	L	G	C	G	S	A	L	1293
TCC	TGG	GAC	CTG	GCC	GAG	GCG	GAA	GTG	GTG	TGT	CAG	CAG	CTG	GGC	TGT	GGC	TCT	GCT	CTG	3906
A	A	L	R	D	A	S	F	G	Q	G	T	G	T	I	W	L	D	D	M	1313
GCT	GCC	CTG	AGG	GAC	GCT	TCG	TTT	GGC	CAG	GGA	ACT	GGA	ACC	ATC	TGG	TTG	GAT	GAC	ATG	3966
R	C	K	G	N	E	S	F	L	W	D	C	H	A	K	P	W	G	Q	S	1333
CGG	TGC	AAA	GGA	AAT	GAG	TCA	TTT	CTA	TGG	GAC	TGT	CAC	GCC	AAA	CCC	TGG	GGA	CAG	AGT	4026
D	C	G	H	K	E	D	A	G	V	R	C	S	G	Q	S	L	K	S	L	1353
GAC	TGT	GGA	CAC	AAG	GAA	GAT	GCT	GGC	GTG	AGG	TGC	TCT	GGA	CAG	TCG	CTG	AAA	TCA	CTG	4086
N	A	S	S	G	H	L	A	L	I	L	S	S	I	F	G	L	L	L	L	1373
AAT	GCC	TCC	TCA	GGT	CAT	TTA	GCA	CTT	ATT	TTA	TCC	AGT	ATC	TTT	GGG	CTC	CTT	CTC	CTG	4146
V	L	F	I	L	F	L	T	W	C	R	V	Q	K	Q	K	H	L	P	L	1393
GTT	CTG	TTT	ATT	CTA	TTT	CTC	ACG	TGG	TGC	CGA	GTT	CAG	AAA	CAA	AAA	CAT	CTG	CCC	CTC	4206
R	V	S	T	R	R	R	G	S	L	E	E	N	L	F	H	E	M	E	T	1413
AGA	GTT	TCA	ACC	AGA	AGG	AGG	GGT	TCT	CTC	GAG	GAG	AAT	TTA	TTC	CAT	GAG	ATG	GAG	ACC	4266

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Fig. 26H

C	L	K	R	E	D	P	H	G	T	R	T	S	D	D	T	P	N	H	G	1433
TGC	CTC	AAG	AGA	GAG	GAC	CCA	CAT	GGG	ACA	AGA	ACC	TCA	GAT	GAC	ACC	CCC	AAC	CAT	GGT	4326
C	E	D	A	S	D	T	S	L	L	G	V	L	P	A	S	E	A	T	K	1453
TGT	GAA	GAT	GCT	AGC	GAC	ACA	TCG	CTG	TTG	GGA	GTT	CTT	CCT	GCC	TCT	GAA	GCC	ACA	AAA	4386
*																				1454
TGA																				4389
CTTTAGACTTCCAGGGCTCACCAGATCAACCTCTAAATATCTTTGAAGGAGACACAACACTTTTAAATGAATAAAGAGGA																				468
AGTCAAGTTGCCCTATGGAAAACCTTGTCCAAATAACATTTCTTGAACAATAGGAGAACACAGCTAAATTGATAAAAGACTGG																				4547
TGATAATAAAAAATTGAATTATGTATATCACTGTTAAAAAATAAAAAAAAAAAAAAAAAACGGACGCGTGGGTCG																				4626
AC																				4628

Fig. 26I

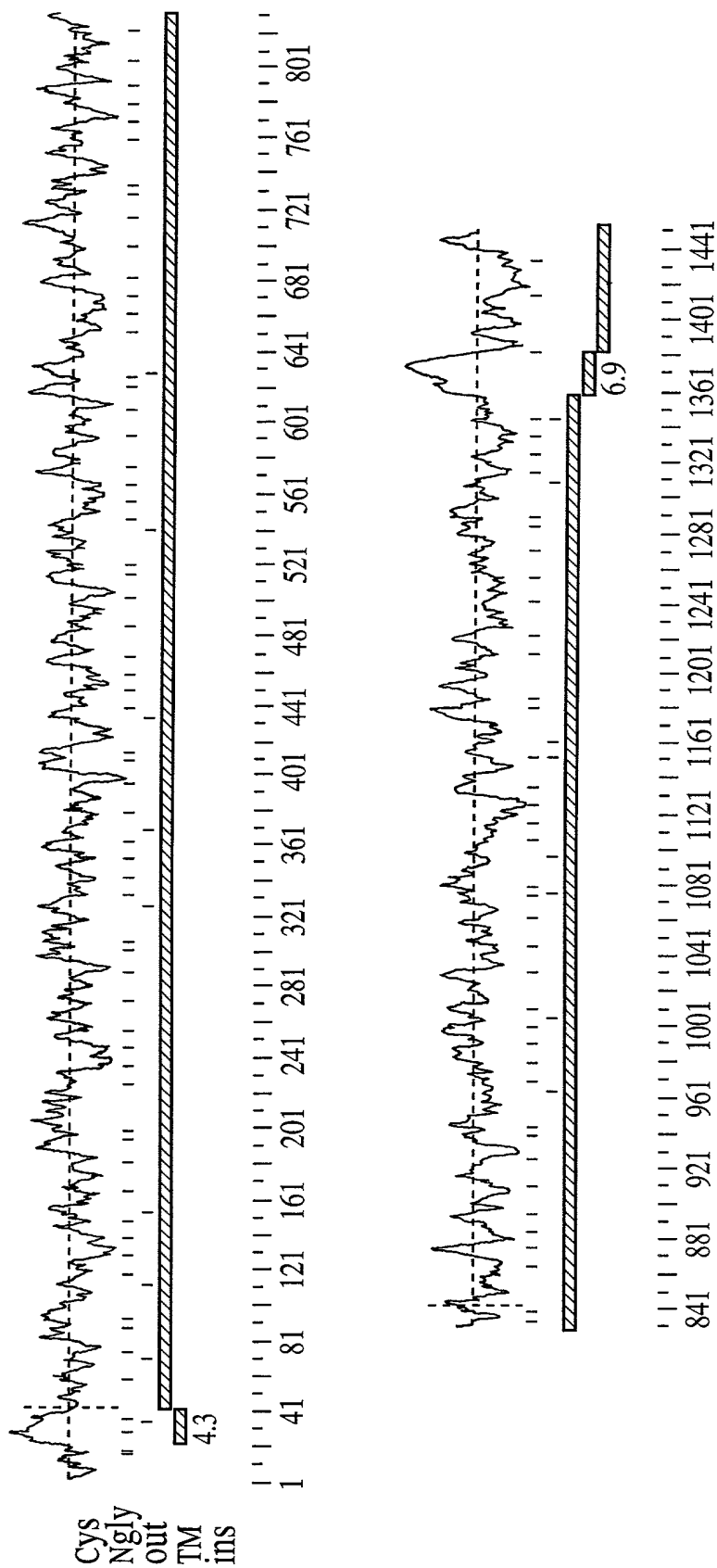


Fig. 26J


```

10      20      30      40      50      60      70
Hum.  MMLPQNSWHIDFGRCCHQNLFSAVVTICILLNSCFLISSFNGTDLELRLVNGDGPCSGTVEVKFQGQWG
      ::      ::      ::      ::      ::      ::      ::
WC1  MAL-----GR---HLSLRGL---CVLLLLGT---MVG---GQALELRLKDGVHRCCEGRVEVKHQGEWG
      10      20      30      40      50

      80      90      100     110     120     130
Hum.  TVCDDGWNTTASTVVCKQLGCPFSFAMFRFGQAVTR-HGKIWLDDVSCYGNESALWECQH---REWGSHN
      ::      ::      ::      ::      ::      ::      ::
WC1  TVDGYRWTLKDASVVCRCQLGCGAAIG-FPGGAYFGPGLPIWLLYTSCEGTESTVSDCEHSNIKDYRNDG
      60      70      80      90     100     110

      140     150     160     170     180     190     200
Hum.  CYHGEDVGVNCYGEANLGLRLVDGNNSCSGRVEVKFQERWGTICDDGWNLTAAVVCRQLGCPSSFISG
      ::      ::      ::      ::      ::      ::      ::
WC1  YNHGRDAGVVCSG-----FVRLAGGDGPCSGRVEVHSGEAWIPVSDGNFTLATAQIICAELGCGKAVSVLG
      120     130     140     150     160     170     180

      210     220     230     240     250     260     270
Hum.  VVNSPAVLRPIWLDDILCQGNELALWNCRHRGWGNHDCSHNEDVTLTCYDSSDLELRLVGTNRCMGRVE
      .      .      .      .      .      .      .
WC1  HELFRESSAQVWAEFFRCEGEPELWVCPRVPCPGTCHHSGSAQVVC SAYSEVRL-MTNGSSQCEGQVE
      190     200     210     220     230     240     250

```

Fig. 26K

```

280      290      300      310      320      330      340
Hum. LKIQRWGTVCHHKWNNAADVCKQLGCGTALHFAGLPHLQSGSDVVWLDGVSCSGNESFLWDCRHS GT
...: ...: ..: ...: ...: ...: ..: ...: ...: ...: ...: ...: ..:
WC1 MNISQWRALCASHWSLANANVICRQLGCGVAISTPGGPHLVEEGDQILTARFHCSCGAESFLWSCPVTAL
260      270      280      290      300      310      320

350      360      370      380      390      400      410
Hum. VNFDCLHQNDVSVICSDGADLELRADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALVVCKQLGCPFSV
. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 GGPDCSHGNTASVICS-GNQI-----QVLPQCND-----SV
330      340      350

420      430      440      450      460      470      480
Hum. FGSRRAKPSNEARDIWINISICTGNESALWDCTYDGKAKRTCRRSDAGVICSDKADLDLRLVGAHSPCY
...: ...: : : : : : : : : : : : : : : : : : : : : : : :
WC1 -----SQPTGSA-----ASEDSA---PY-----CSDSRQL--RLVDGGGPCA
360      370      380

490      500      510      520      530      540      550
Hum. GRLEVKYQGEWGTVCHDRWSTRNAADVCKQLGCGKPMHVFGMTYFKEASGPIWLDDVSCIGNESNIWDCE
...: ...: ...: ...: ..: ...: ...: ...: ...: ...: ...: ...: :
WC1 GRVEILDQGSWGTICDDGWDLDDARVVCRQLGCGEALNATGSAHFGAGSGPIWLDNLNCTGKESHVWRCP
390      400      410      420      430      440      450

```

Fig. 26L

560	570	580	590	600	610	620
Hum.	HS	GW	GK	HN	CV	HR
ED	VI	TC	SG	DA	TW	GL
RL	VG	GS	NR	CS	GR	LE
VF	YF	QGR	WT	VC	DD	GW
NS	KA	AA	AV	VC	SL	DC
WC1	SR	GW	QH	NC	RH	KD
AG	VI	CS	--	EF	LA	RM
VS	ED	QQ	CA	GW	LE	VF
YNG	TW	GS	VC	RN	PM	ED
IT	VS	TI	CR	QL	GC	
460	470	480	490	500	510	520
Hum.	PS	SI	IG	ML	GN	AS
TG	YK	IW	LD	VS	CD	GE
SD	LS	CR	NS	GW	NN	DC
SH	SE	DV	GS	IC	SD	AS
DM	EL	RL	VG	GS		
WC1	GD	SG	TL	NS	SV	AL
RE	GP	QW	DR	IQ	CR	KT
DT	SL	WQ	CP	SD	PN	YN
SC	SP	KE	AY	IC	AD	SR
--	QI	RL	VD	GG		
530	540	550	560	570	580	590
Hum.	700	710	720	730	740	750
760	SR	CAG	KE	VN	VQ	GA
VG	IL	CAN	GW	MN	IA	EV
VC	RQ	LE	CG	SA	IR	VS
RE	PH	FT	ER	TL	HI	LM
SN	SG	CT	GG	EA	SL	
WC1	GR	CS	GR	VE	IL	DQ
GS	WT	IC	DD	RD	LD	DA
RV	CK	QL	GC	GE	AL	DA
TV	SS	FF	GT	GS	GP	IW
LD	EV	NC	RG	EE	SQ	
600	610	620	630	640	650	660
Hum.	770	780	790	800	810	820
830	WD	CI	RE	WK	QT	AC
HL	NE	AS	LI	CS	AH	RQ
PR	LV	GA	DM	PC	SG	RV
EH	KA	DT	WR	SV	CD	SD
FL	HA	AN	VL	CR	EL	
WC1	WR	CP	SW	GR	QH	CN
QH	ED	AG	VI	CS	GF	--
VR	LA	GG	DP	CS	GR	VE
VS	HS	GE	AW	TP	VS	DN
FT	LP	TA	QV	IC	AE	
670	680	690	700	710	720	730

Fig. 26M

Figure 26N

Hum.	840	850	860	870	880	890	900
	NCGDAISLSVGDHFGKGNGLTWAEEKFQCEGSETHALCPIVQHPEDTCIHSREVGVCYSRYTDVRLV-NG						
WC1	740	750	760	770	780	790	800
	GCGKAVSVLGHMPFRESDGQVWAEFFRCDCGGEPELWSCPRVPCGGTCLHSGAAQVVCVSVYTEVQLMKNG						
Hum.	910	920	930	940	950	960	970
	KSQCDGQVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTGGKYIGERSVRVWGHFRFHCIGNESL						
WC1	810	820	830	840	850	860	870
	TSQCEGQVEMKISGRWRALCASHWSLANANVCRQLGCGVAISTPRGPHLVEGDDQISTAQFHCSGAESF						
Hum.	980	990	1000	1010	1020	1030	1040
	LDNCQMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLSAVPEGSALICLEDKRLRLVDGDSRC						
WC1	880	890	900	910	920	930	940
	LWSCPVTALGGPDCSHGNTASVICSGNHTQVLPQCNDFLSQPAGSAASEESSPYCSDSRQLRLVDGGGPC						
Hum.	1050	1060	1070	1080	1090	1100	1110
	AGRVEIYHDGFWGTICDDGWDLSDAHVVQCQLGCGVAFNATVSAHFGECSGPIWLDDLNCTGTESHLWQC						
WC1	950	960	970	980	990	1000	1010
	GGRVEILDQGSWGTICDDDWLDDARVVCRLGCGEALNATGSAHFGAGSGPIWLDDLNCTGKESHVWRC						

Fig. 26N

```

1120      1130      1140      1150      1160      1170      1180
Hum.  PSRWGQHDCRHKEDAGVICSEFTALRLYSETETESCAGRLEVFYNGTWGSVGRNITTAIAGIVCRQLG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  PSRWGHRHDCRHKEDAGVICSEFLALRMVSEDQQ--CAGWLEVFYNGTWGSVCRSPMEDITVSVICRQLG
      1020      1030      1040      1050      1060      1070

1190      1200      1210      1220      1230      1240
Hum.  CGENGVS LAPLSKTGSGFMWDDIQCPKTHISIWQCL SAPWERRISSPAEETWITCEDR-----
      : : : : . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  CGDSGSLNTSVGLREGSRPRWVDLIQCRKMDTSLWQCPSPGWKYSSCPKEEAYISCEGRRPKSCPTAAA
1080      1090      1100      1110      1120      1130      1140

1250      1260      1270      1280      1290      1300
Hum.  -----IRVRGGDTECSGRVEIWHAGSWGTVCDSDWDLAEAEVVCQQLGCGSALAALRDASFQGTGTIW
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  CTDREKLRLRGGDSECSGRVEVWHNGSWGTVCDSDWSLAEAEVVCQQLGCGQALEAVRSAAFPGNGSIW
1150      1160      1170      1180      1190      1200      1210

1310      1320      1330      1340      1350      1360
Hum.  LDDMRCKGNESFLWDCHAKPWGQSDCGHKEDAGVRCSG-----QSLKSLNASSGHLALI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  LDEVQCGGRESSLWDCVAEPWGQSDCKHEEDAGVRCSGVRTTLPTTTAGTRTTSNLSLPGIFSLPGVLC LI
1220      1230      1240      1250      1260      1270      1280

```

Fig. 260

```

1370      1380      1390      1400      1410
Hum.  LSSIFGLLLVLFIFLTWCVRVQK-----QKHLPLRVS-----TRRRG-----SLEENLFHEME
      :...: :...: . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  LGSLLFLVLVILVTQLLRW-RAERRALSSYEDALAEAVYEELDYLLTQKEGLGSPDQMTDVPDENYDDAE
1290      1300      1310      1320      1330      1340      1350

      1420      1430      1440
Hum.  TC-----LKREDPHGTRTSD-----DTPNHGCEDAS-----DTSLLGV
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  EVPVPGTPSPSQNGEEFVPEKEDGVRSSQTGSFLNFSREANPGEGEESFWLLQKKGDAGYDDVELSA
1360      1370      1380      1390      1400      1410      1420

      1450
Hum.  LPASEAT-K
      : : : :
WC1  LGTSPVTFS
1430

```

Fig. 26P

Fig. 26Q-1

```

280      290      300      310      320      330      340
Hum. TCCTTCGCCATGTTTCGTTTTGGACAAGCCGTGA--CTAGACATGGAAAAATTGGCCTTGATGATGTTTC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GCCATTG--GTTTTCCCTGGAGGGGCTTATTTTGGGCCAGGACTTGGCCCCCATTTGGCCTTTTGTATACTTC
220      230      240      250      260      270      280
      350      360      370      380      390      400      410
Hum. CTGTTATGGAATGAGTCAGCTCTCTGGGAATGTCAACACCCGGGAATGGGGAAGCCATAACTGTTATCAT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  ATGTGAAGGACAGAGTCAACTGTGAGTGTGAGCAT-TCTAATATTAAAGAC-TATC-GTAATGAT
290      300      310      320      330      340      350

420      430      440      450      460      470      480
Hum. GGAGAAGATGTTGGTGTGAACGTGTTATGTTGAAGCCAA-TCTGGGTTTGAG--GCTAG-TGGATGGAAC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GGCTATAATCATGGTCGGGA---TGCTGGAGTAGTCTGCTCAGGATTTGTGCGTCTGGCTGGAGGGGATG
360      370      380      390      400      410      420

490      500      510      520      530      540      550
Hum. AACTCCTGTTCAAGGGAGAGTGGAGGTGAAAATTCCAAGAAAGGTGGGGGACTATATGTGATGATGGGTGGA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GAC-CCTGCTCAGGGCGAGTAGAAGTGCAATT--CTGGAGAAGCTTGGATCCCAGTGT-CTGATGGGAACT
430      440      450      460      470      480

```

Fig. 26Q-2


```

560      570      580      590      600      610      620
Hum.  ACTTGAA TACTGCTGCCGTGGTGTGCAGGCAACTAGGATGTCCATCTTCTTTATTCTTCTGGAGTTGT
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
WC1   TCACACTTGCCACTGCC-----CAG-----ATCATCTGT-----GCAGAGTTGGG
490      500      510      520

630      640      650      660      670      680      690
Hum.  TAATAGCCCTGCTGTATTGCGCCCATTTGGCTGGATGACATTTATGCCAGGGAATGAGTTGGCACT-
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   TTGTGGC-----AAGGCTG--TGTCGT-----CCTGGGACATGAG----CTCTT
530      540      550      560

700      710      720      730      740      750      760
Hum.  CTGGAATTGCAGACATCGTGGATGGGAAATCATGACTGCAGTCACAATGAGGATGTCACATTAACTTGT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   CAGAGAGTCCAGT-GCC-----CAGGTCTG--GGC---TGAAGAGTTCA-----GG
570      580      590      600

770      780      790      800      810      820      830
Hum.  TATGATAGTAGTGATCTTGAACTAAGGCTTGTAGGTGGAACCTAACCGCTGTATGGGAGAGTAGAGCTGA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   TGTGAGGGGGAGGAGCCTGAGCT---CT-----GGGTCTGCCC-CAGAGTG-----CCCTG-
610      620      630      640      650

```

Fig. 26Q-3

```

      840      850      860      870      880      890      900
Hum.  AAATCCAAGGAGGTGGGGACCGTATGCCACCATAAGTGGAACAATGCTGCAGCTGATGTCGTATGCAA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  ---TCCA-----GGGGGCACGTGT--CACCACA-GTGGATC--TGCT-CAGGTTGTTTGTTCAGCAT
      660      670      680      690      700

      910      920      930      940      950      960      970
Hum.  GCAGTTGGGATGTGGAACCGCACTTCACCTCGCTGGCTTGCCCTCATTTGCAGTCAGGGTCTGATGTTGTA
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  ACT-----CAGAAGTCCGGCTCATGACAA-AC-GGCT--CCTC-TCAG-TGTGAAGGGCAGGTGGAGAT
      710      720      730      740      750      760

      980      990      1000      1010      1020      1030      1040
Hum.  TGGCTTGATGGTGTCTCCTGCTCCGGTAATGAATCTTTCTTTGGGACTGCAGACATTCGGGAACCGTCA
      . . . . . : : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GAACATT-----TCTG-GACAATGGAGAGCGCTCTGTGCCTCCC-ACTGGAGTCTGGCCAAATGCC---A
      770      780      790      800      810      820

      1050      1060      1070      1080      1090      1100      1110
Hum.  ATTTTGACTGTCTTCATCAAAAACGATGTGTCTGTGATCTGCTCAGATGGAGCAGATTTGGAACCTGCGACT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  ATGTTATCTGTCAGCTCGGCTGTGGAGTTGCCATCTCCACCCCGGAG-----GACCAC-ACT
      830      840      850      860      870      880

```

Fig. 26Q-4

	1120	1130	1140	1150	1160	1170	1180
Hum.	AGCAGATGGAAGTAACAATTGTT	CAGGAGAGTAGAGGTGAGAATTCA	TGAACAGTGGTGGACAATATG				
	:: ::::::::::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::
WC1	TG---GTGGAAGAAG--	GTGATCAG--ATCCTAACAGCCCCGATT	TCACTGCTCTG---GGGC----	TG			
	890	900	910	920	930		
	1190	1200	1210	1220	1230	1240	1250
Hum.	TGACCAGAACTGGAAGAAATGAACAAGCCCTT	GTGTTTGTAAAGCAGCTAGGATGTCCGTT	CAGCGTCTTT				
	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::
WC1	AGTCCT-TCCTGTGGAGTTGT-----	CCT-GTGACT-----GCC-CTGGGTGTCCTGACTGT	TCCCAT				
	940	950	960	970	980	990	
	1260	1270	1280	1290	1300	1310	1320
Hum.	GGCAG-TCGTCGTGCTAAACCTAGTAATGAAGCT	AGAGACATTTGGATAAACAGCATAATCT	TGCAC	TGGG			
	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::
WC1	GGCAACACAGCCCTCTGTGATCTGCTCAGGAAAC	CAGATCCAGGTGCTTCCCCCAGTGCAACGA-CT	CCG--				
	1000	1010	1020	1030	1040	1050	1060
	1330	1340	1350	1360	1370	1380	1390
Hum.	AATGAGTCAGCTCTCTGGACTGCACATATGAT	GGAAAGCAAGCGAACATGCTTCCGAAGAT	CAGATG				
	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::
WC1	--TGCTCAACCTACAGGCTCTGC-----	GGC-----CTCAGAGGACA-GCGCCC-----	CCTACTG				
	1070	1080	1090	1100			

Fig. 26Q-5

Fig. 26Q-6

```

1670      1680      1690      1700      1710      1720      1730
Hum. ACACAGTGGATGGGAAAGCATAATTGTGTACACAGAGAGGATGTGATTGTAACCTGCTCAGGTGATGCA
. : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 TTCCCGGGCTGGGGCAGCACAACTGCAGACACAAAGCAGGACGCGGGGTCATCTGCTCAG--AGTTC-
1370      1380      1390      1400      1410      1420      1430

1740      1750      1760      1770      1780      1790      1800
Hum. ACATGGGGCCCTGAGGCTGGTGGGGCGGAGCAACCGCTGCTCGGGAAGACTGGAGGTGTACTTTCAAGGAC
. : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 -CT--GGCCCTCAGGATGGTGAGTGAGGACCAAGCAGTGTGCTGGTGGCTGGAAGTTTCTACAAATGGGA
1440      1450      1460      1470      1480      1490      1500

1810      1820      1830      1840      1850      1860      1870
Hum. GGTGGGCACAGTGTGTGATGACGGCTGGAACAGTAAAGCTGCAGCTGTGGTGTAGCCAGCTGGACTG
. : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 CCTGGGCAGTGTCTGCCGTAACCCCATGGAAGACATCACTGTGTCCACGATCTGCAGACAGCTTGGCTG
1510      1520      1530      1540      1550      1560      1570

1880      1890      1900      1910      1920      1930      1940
Hum. CCCATCTTCTATCATTTGGCATGGGCTCTG-GGAAACGCTTCTA-CAGGATATGGAAAAATTTGGCTCGATG
. : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 T--GGGGACAGTGGAAACCCCTCAACTCTTCTGTGCTCTTAGAGAAGGTTTATAGGCCACAGTGGGTGGAT-
1580      1590      1600      1610      1620      1630

```

Fig. 26Q-7

Hum.	1950	1960	1970	1980	1990	2000	2010
WC1	1640	1650	1660	1670	1680	1690	1700
Hum.	2020	2030	2040	2050	2060	2070	2080
WC1	1710	1720	1730	1740	1750	1760	
Hum.	2090	2100	2110	2120	2130	2140	2150
WC1	1770	1780	1790	1800	1810	1820	1830
Hum.	2160	2170	2180	2190	2200	2210	2220
WC1	1840	1850	1860	1870	1880	1890	1900

Fig. 26Q-8

Fig. 26Q-9

Fig. 26Q-10

Fig. 26Q-11

	3060	3070	3080	3090	3100	3110	3120
Hum.	ATATTGCTGCAGTTC	CAGAGGCAGTGT	TGATCTGTAGAG	CAAAACGGCTCC	GCCTAGTGGAT		

WC1	TGCAGGCTCTCGGCC	CTCAGAGAGATT	CTCCCTACTGCT	CAGACAGCAGG	CAGCTCCGCC	CTGGTGGAC	
	2740	2750	2760	2770	2780	2790	2800
	3130	3140	3150	3160	3170	3180	3190
Hum.	GGGACAGCCGCTGT	GCCCCGAGAGAT	CTATCACGACGG	CTTCTGGGGCACC	ATCTGTGATGACG		

WC1	GGGGCGGTCCCTG	CGCGGAGAGTGG	AGATCCTTGACC	AGGGCTCCTGGG	GCACCATCTGTG	ATGATGATG	
	2810	2820	2830	2840	2850	2860	2870
	3200	3210	3220	3230	3240	3250	3260
Hum.	GCTGGACCTGAGCG	ATGCCACGTTGG	TGTCAAAAGCTG	GGCTGTGGAGTG	GCCTTCAATGCC	ACGGT	

WC1	ACTGGACCTGGACG	ATGCCCGTGTGT	GCAGGCAGCTGG	GGCTGTGGAGA	AGCCCTCAATG	CCACGGG	
	2880	2890	2900	2910	2920	2930	2940
	3270	3280	3290	3300	3310	3320	3330
Hum.	CTCTGCTCACTTTG	GGGAGGGGTCA	GGGCCCCATCT	GGCTGGATGACC	TGAACGCACAG	GGAACGGAGTCC	

WC1	GTCTGCTCACTTC	GGGGCAGGATC	AGGGCCCCATC	TGGCTGGACGAC	CCTGAACGCAC	AGGAAGGAGTCC	
	2950	2960	2970	2980	2990	3000	3010

Fig. 26Q-12

```

3340      3350      3360      3370      3380      3390      3400
Hum.  CACTTGTGCAGTGCCCTTCCCGCGGCTGGGGCAGCACGACTGCAGGCACAAGGAGGACGCGAGGGGTCA
      ::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
WC1   CACGTGTGGAGGTGCCCTTCCCGGGGCTGGGGCGGCACGACTGCAGACACACAAGGAGGACGCCGGGGTCA
      3020      3030      3040      3050      3060      3070      3080

3410      3420      3430      3440      3450      3460      3470
Hum.  TCTGCTCAGAAATTCACAGCCCTTGAGGCTCTACAGTGAAACTGAAACAGAGAGCTGTGCTGGGAGATTGGA
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
WC1   TCTGCTCAGAGTTCCCTGGCCCTCAGGAT----GGTGAG-CGAGGACCCAGCAG-TGTGCTGGGTGGCTGGA
      3090      3100      3110      3120      3130      3140

3480      3490      3500      3510      3520      3530      3540
Hum.  AGTCTTCTATAACGGGACCTGGGGCAGCGTCGGCAGGAGGAACATCACACAGCCATAGCAGGCATTGTG
      ::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
WC1   GGTTTTCTACAACGGGACCTGGGGCAGTGTCTGCCGCGAGCCCCCATGGAAGATATCACTGTGTCCGTGATC
      3150      3160      3170      3180      3190      3200      3210

```

Fig. 26Q-13

Fig. 26Q-14

[illegible]

Fig. 26Q-15

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3910      3920      3930      3940      3950      3960      3970
Hum.  GGAAC TGGAA CCA TCTGG TTGAT GACAT GCGGT GCAA AAGAA ATGAG TCATT CTAT GGGAC TGTCA CG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   GGAAT TGGAG CATCTGG CTGGA CAGAG GTGCA GTGCG GGGCC GGGAG TCCCT GTTGG GACTGTG GTTG
3640      3650      3660      3670      3680      3690      3700

3980      3990      4000      4010      4020      4030      4040
Hum.  CCAAA CCTT GGGAC AGAGT GACTG TGGAC ACAAG GAAGAT GCTGG CGTG AGGTG CTCTG G---ACAGTC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   CGGAG CCC TGGGG CAGAG CGGAC TGCAA AGCAC GAGAG GATG CTGGT GTGAG GTGCT CTGGT GTAA GGCAC
3710      3720      3730      3740      3750      3760      3770

4050      4060      4070      4080      4090
Hum.  G----- CTGAA AATCA CTA TGAAT G---CCT -----CCTCAGGT-CATT---TAGCA-CTTATTTATCCA
      . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   AACATTG CCCCAC GACCA CAGCA GGGAC CAGAA CAACTCAA AATTCTCTCCCTGGCATCTTCTCCCTGCCT
3780      3790      3800      3810      3820      3830      3840

```

Fig. 26Q-16

Fig. 26Q-17

```

4230
Hum. ---GATGGAG-----ACCTG-----CCTC-----AAGAGAGAGGAC
      :::::      :::::      :::::      :::::      :::::
WC1 TATGATGATGCTGAAGAAGTACCAGTGCCTGGAACCTCTTCTCCCTCTCAGGGGAATGAGGAGGAAGTGC
4060 4070 4080 4090 4100 4110 4120

4260 4270 4280 4290
Hum. CCACATGGGACAAAGAAC-----CTCAGA-TGACAC---CC-----CCAA-----
      :: :: :::: ::::: ::::: ::::: ::::: :::::
WC1 CCCACAGAGAAGGAGGACGGGTGAGGTCCTCTCAGACAGGCTCTTCTGAACTTCTCCAGAGAGCAGC
4130 4140 4150 4160 4170 4180 4190

4300 4310 4320 4330
Hum. ---CCATGGTT--GTGAAGA---TGCTAGCGACAC-----ATCGCTG--TTGGGAGTT
      :: :: . ::::: : ::::: ::::: .. ::::: . :::::
WC1 TAATCCTGGGGAAGGAGAAGAGAGCTTCTGGCTGCTCCAGGGGAAGAAAGGGATGCTGGGTATGATGAT
4200 4210 4220 4230 4240 4250 4260

```

Fig. 26Q-18

4340

Hum. CTT-----CCTG-----CCTCTGAAGCCACAAAA

4350

WC1 GTTGAAC TCAGT GCCCCTGGGGAACATCCCCAGT TTTCTCG

4270 4280 4290 4300

Fig. 26Q-19

GTCGACCCACGCGTCCGGTCTGTGGCTGAGC	M	A	L	P	A	L	G	L	D	P	W	S	12
	ATG	GCC	CTC	CCA	GCC	CTG	GGC	CTG	GAC	CCC	TGG	AGC	67
L L G L F L F L Q L L Q L L L P T T A G													32
CTC CTG GGC CTT TTC CTC TTC CAA CTG CTT CAG CTG CTG CCG ACG ACG ACC GCG GGG													127
G G G Q G P M P R V R Y Y A G D E R A													52
GGA GGC GGC CAG GGC CCC ATG CCC AGG GTC AGA TAC TAT GCA GGG GAT GAA CGT AGG GCA													187
L S F F H Q K G L Q D F D T L L L S G D													72
CTT AGC TTC TTC CAC CAG AAG GGC CTC CAG GAT TTT GAC ACT CTG CTC CTG AGT GGT GAT													247
G N T L Y V G A R E A I L A L D I Q D P													92
GGA AAT ACT CTC TAC GTG GGG GCT CGA GAA GCC ATT CTG GCC TTG GAT ATC CAG GAT CCA													307
G V P R L K N M I P W P A S D R K K S E													112
GGG GTC CCC AGG CTA AAG AAC ATG ATA CCG TGG CCA GCC AGT GAC AGA AAA AAG AGT GAA													367
C A F K K K S N E T Q C F N F I R V L V													132
TGT GCC TTT AAG AAG AAG AGC AAT GAG ACA CAG TGT TTC AAC TTC ATC CGT GTC CTG GTT													427
S Y N V T H L Y T C G T F A F S P A C T													152
TCT TAC AAT GTC ACC CAT CTC TAC ACC TGC GGC ACC TTC GCC TTC AGC CCT GCT TGT ACC													487
F I E L Q D S Y L L P I S E D K V M E G													172
TTC ATT GAA CTT CAA GAT TCC TAC CTG TTG CCC ATC TCG GAG GAC AAG GTC ATG GAG GGA													547

Fig. 27A

GenBank

K	G	Q	S	P	F	D	P	A	H	K	H	T	A	V	L	V	D	G	M	192
AAA	GGC	CAA	AGC	CCC	TTT	GAC	CCC	GCT	CAC	AAG	CAT	ACG	GCT	GTC	TTG	GTG	GAT	GGG	ATG	607
L	Y	S	G	T	M	N	N	F	L	G	S	E	P	I	L	M	R	T	L	212
CTC	TAT	TCT	GGT	ACT	ATG	AAC	AAC	TTC	CTG	GGC	AGT	GAG	CCC	ATC	CTG	ATG	CGC	ACA	CTG	667
G	S	Q	P	V	L	K	T	D	N	F	L	R	W	L	H	H	D	A	S	232
GGA	TCC	CAG	CCT	GTC	CTC	AAG	ACC	GAC	AAC	TTC	CTC	CGC	TGG	CTG	CAT	CAT	GAC	GCC	TCC	727
F	V	A	A	I	P	S	T	Q	V	V	Y	F	F	F	E	E	T	A	S	252
TTT	GTG	GCA	GCC	ATC	CCT	TCG	ACC	CAG	GTC	GTC	TAC	TTC	TTC	TTC	GAG	GAG	ACA	GCC	AGC	787
E	F	D	F	F	E	R	L	H	T	S	R	V	A	R	V	C	K	N	D	272
GAG	TTT	GAC	TTC	TTT	GAG	AGG	CTC	CAC	ACA	TCG	CGG	GTG	GCT	AGA	GTC	TGC	AAG	AAT	GAC	847
V	G	G	E	K	L	L	Q	K	K	W	T	T	F	L	K	A	Q	L	L	292
GTG	GGC	GGC	GAA	AAG	CTG	CTG	CAG	AAG	AAG	TGG	ACC	ACC	TTC	CTG	AAG	GCC	CAG	CTG	CTC	907
C	T	Q	P	G	Q	L	P	F	N	V	I	R	H	A	V	L	L	P	A	312
TGC	ACC	CAG	CCG	GGG	CAG	CTG	CCC	TTC	AAC	GTC	ATC	CGC	CAC	GCG	GTC	CTG	CTC	CCC	GCC	967
D	S	P	T	A	P	H	I	Y	A	V	F	T	S	Q	W	Q	V	G	G	332
GAT	TCT	CCC	ACA	GCT	CCC	CAC	ATC	TAC	GCA	GTC	TTC	ACC	TCC	CAG	TGG	CAG	GTT	GGC	GGG	1027
T	R	S	S	A	V	C	A	F	S	L	L	D	I	E	R	V	F	K	G	352
ACC	AGG	AGC	TCT	GCG	GTT	TGT	GCC	TTC	TCT	CTC	TTG	GAC	ATT	GAA	CGT	GTC	TTT	AAG	GGG	1087

Fig. 27B

K	Y	K	E	L	N	K	E	T	S	R	W	T	T	Y	R	G	P	E	T	372
AAA	TAC	AAA	GAG	TTG	AAC	AAA	GAA	ACT	TCA	CGC	TGG	ACT	ACT	TAT	AGG	GGC	CCT	GAG	ACC	1147
N	P	R	P	G	S	C	S	V	G	P	S	S	D	K	A	L	T	F	M	392
AAC	CCC	CGG	CCA	GGC	AGT	TGC	TCA	GTG	GGC	CCC	TCC	TCT	GAT	AAG	GCC	CTG	ACC	TTC	ATG	1207
K	D	H	F	L	M	D	E	Q	V	V	G	T	P	L	L	V	K	S	G	412
AAG	GAC	CAT	TTC	CTG	ATG	GAT	GAG	CAA	GTG	GTG	GGG	ACG	CCC	CTG	CTG	GTG	AAA	TCT	GGC	1267
V	E	Y	T	R	L	A	V	E	T	A	Q	G	L	D	G	H	S	H	L	432
GTG	GAG	TAT	ACA	CGG	CTT	GCA	GTG	GAG	ACA	GCC	CAG	GGC	CTT	GAT	GGG	CAC	AGC	CAT	CTT	1327
V	M	Y	L	G	T	T	T	G	S	L	H	K	A	V	V	S	G	D	S	452
GTC	ATG	TAC	CTG	GGA	ACC	ACC	ACA	GGG	TCG	CTC	CAC	AAG	GCT	GTG	GTA	AGT	GGG	GAC	AGC	1387
S	A	H	L	V	E	E	I	Q	L	F	P	D	P	E	P	V	R	N	L	472
AGT	GCT	CAT	CTG	GTG	GAA	GAG	ATT	CAG	CTG	TTC	CCT	GAC	CCT	GAA	CCT	GTT	CGC	AAC	CTG	1447
Q	L	A	P	T	Q	G	A	V	F	V	G	F	S	G	G	V	W	R	V	492
CAG	CTG	GCC	CCC	ACC	CAG	GGT	GCA	GTG	TTT	GTA	GGC	TTC	TCA	GGA	GGT	GTC	TGG	AGG	GTG	1507
P	R	A	N	C	S	V	Y	E	S	C	V	D	C	V	L	A	R	D	P	512
CCC	CGA	GCC	AAC	TGT	AGT	GTC	TAT	GAG	AGC	TGT	GTG	GAC	TGT	GTC	CTT	GCC	CGG	GAC	CCC	1567
H	C	A	W	D	P	E	S	R	T	C	C	L	L	S	A	P	N	L	N	532
CAC	TGT	GCC	TGG	GAC	CCT	GAG	TCC	CGA	ACC	TGT	TGC	CTC	CTG	TCT	GCC	CCC	AAC	CTG	AAC	1627

Fig. 27C

S W K Q D M E R G N P E W A C A S G P M 552
TCC TGG AAG CAG GAC ATG GAG CGG GGG AAC CCA GAG TGG GCA TGT GCC AGT GGC CCC ATG 1687

S R S L R P Q S R P Q I I K E V L A V P 572
AGC AGG AGC CTT CGG CCT CAG AGC CGC CCG CAA ATC ATT AAA GAA GTC CTG GCT GTC CCC 1747

N S I L E L P C P H L S A L A S Y Y W S 592
AAC TCC ATC CTG GAG CTC CCC TGC CCC CAC CTG TCA GCC TTG GCC TCT TAT TAT TGG AGT 1807

H G P A A V P E A S S T V Y N G S L L L 612
CAT GGC CCA GCA GTC CCA GAA GCC TCT TCC ACT GTC TAC AAT GGC TCC CTC TTG CTG 1867

I V Q D G V G G L Y Q C W A T E N G F S 632
ATA GTG CAG GAT GGA GTT GGG GGT CTC TAC CAG TGC TGG GCA ACT GAG AAT GGC TTT TCA 1927

Y P V I S Y W V D S Q Q D Q T L A L D P E 652
TAC CCT GTG ATC TCC TAC TGG GTG GAC AGC CAG CAG GAC CAT CCG TTG ACC AGG GTC AGT GGT GGC GAA 1987

L A G I P R E H V K V P L T R V S G G A 672
CTG GCA GGC ATC CCC CGG GAG CAT GTG AAG GTC CCG TTG ACC AGG GTC AGT GGT GGC GGC 2047

A L A A Q Q S Y W P H F V T V T V L F A 692
GCC CTG GCT GCC CAG CAG TCC TAC TGG CCC CAC TTT GTC ACT GTC ACT GTC CTC TTT GCC 2107

L V L S G A L I I L V A S P L R A L R A 712
TTA GTG CTT TCA GGA GCC CTC ATC ATC CTC GTG GCC TCC CCA TTG AGA GCA CTC CGG GCT 2167

Fig. 27D

R	G	K	V	Q	G	C	E	T	L	R	P	G	E	K	A	P	L	S	R	732
CGG	GGC	AAG	GTT	CAG	GGC	TGT	GAG	ACC	CTG	CGC	CCT	GGG	GAG	AAG	GCC	CCG	TTA	AGC	AGA	2227
E	Q	H	L	Q	S	P	K	E	C	R	T	S	A	S	D	V	D	A	D	752
GAG	CAA	CAC	CTC	CAG	TCT	CCC	AAG	GAA	TGC	AGG	ACC	TCT	GCC	AGT	GAT	GTG	GAC	GCT	GAC	2287
N	N	C	L	G	T	E	V	A	*											762
AAC	AAC	TGC	CTA	GGC	ACT	GAG	GTA	GCT	TAA											2317
ACT	CTA	GGC	CAC	AGG	CGG	TGC	AGG	CAC	CTG	GGC	ATG	CTG	GGC	GGC	CC	AA	GCA	CAG	CCCT	2396
TGAC	AGC	AGC	ACAA	AGAC	CACT	TTCT	CCCC	TGAG	AGG	AGCT	TTCT	GCT	ACT	CTG	CAT	CACT	GAT	GAC	ACT	2475
TGAT	GCA	AGC	AGT	CTG	CCCT	ATG	GGAC	TCCCT	TTCT	ACCA	GCAT	GAG	CTCT	CTA	AC	AGG	TGG	GGCT	ACCC	2554
CCAG	ACCT	GTCT	CTAC	ACT	GAT	ATT	GA	GA	AACT	GGAG	AGG	ATCCT	TCA	GTCT	GGCC	ATTC	CAG	GGAC	CCCT	2633
CAC	AGT	TTCA	AGAT	CTA	AAAA	AACT	GCCT	GTCC	CAG	ACCT	ATG	TAAT	GA	AC	CA	CA	AA	CA	ATCT	2712
ATAT	GCTA	ACAT	GCC	ACT	CTG	AACT	CCACT	CTGA	AGCT	GCCG	TTTG	GAC	ACCA	CACT	CCCT	TTCT	CCC	AGG	GTCA	2791
TGC	AGG	ATCT	GTCT	CCCT	TTACC	AGT	CGT	GCAC	CGCT	GACT	CCC	AGG	AGT	CTTT	CCT	GAA	GTCT	GACC		2870
ACCT	TTCT	TTCT	TTG	CTT	CAG	TTGG	GCAG	ACT	CTG	ATCC	CTT	CGCC	TGG	CAG	AGG	TAAT	CTG	AGC	CTTCT	2949
TCAC	TCCT	TTAC	CCCT	AGCT	CTCC	CCCT	CTCC	CTCC	CTCC	CTCC	CTCC	CTCC	CTCC	CTCC	CTCC	CTCC	CTCC	CTCC	CTCC	3028
AGAG	ACT	GTTT	ATTT	TTT	TTA	TTA	TTA	TTA	TTA	TTA	TTA	TTA	TTA	TTA	TTA	TTA	TTA	TTA	TTA	3104

Fig. 27E

Fig. 27F

Figure 27H

Hum.	570	580	590	600	610	620	630
	RPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLLVQDGVGGLYQCWATENG						

Mur.	560	570	580	590	600	610	620
	PPQLIKEVLTVPNSILELRCPHLSALASYWSHGGRAKISEASATVYNGSLLLLPQDGVGGLYQCVATENG						

Hum.	640	650	660	670	680	690	700
	FSYPVISYWVDSQDQTLALDPELAGIPREHVKVPPLTRVSGGAALAAQQSYWPHFVTVTLFALVLSGALI						

Mur.	630	640	650	660	670	680	690
	YSYPVVSYWVDSQDQPLALDPELAGVPRERVQVPLTRVGGGASMAAQRSYWPFLIVTVLLAIVLLGVLT						

Hum.	710	720	730	740	750	760	
	ILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCGLTEVA						

Mur.	700	710	720	730	740	750	760
	LLLASPLGALRARGKVQGCGLPFPREKAPLSRDQHLQPSKDHRTSASDVDADNHHLGAEVA						

Fig. 27H

[illegible]

Fig. 27I

Fig. 27J

	530	540	550	560	570	580	590
Hum.	GGAGACAAGGTCAATGGAGGAAAGGCCAAAGCCCCCTTTGACCCCGCTCACAAGCATACG-GCTGTCTT						

Mur.	GATAGACAAGGTCAATGGACGGGAAAGGCCAAAGCCC-TTTGACCCCTGTTCAACAAGCACACAAGCTGTCTT						
	560	570	580	590	600	610	620
	600	610	620	630	640	650	660
Hum.	GGTGGATGGGATGCTCTATTCTGGTACTATGAACAACCTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACA						
	::: ::
Mur.	GGTCGATGGGATGCTTTATTCCGGCACCATGAACAACCTTCCTGGGCAGCGAGCCCATCCTGATGCGGACACA						
	630	640	650	660	670	680	690
	670	680	690	700	710	720	730
Hum.	CTGGGATCCCAGCCTGTCCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCATGACGCCCTCCTTTGTGG						
	::
Mur.	CTGGGATCCCAGCCTGTTCCTCAAGACTGACATCTTCTTACGCTGGCTGCACGCGGATGCCCTCCTTCGTGG						
	700	710	720	730	740	750	760
	740	750	760	770	780	790	800
Hum.	CAGCCATCCCCTTCGACCCAGGTCGTCCTACTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGA						

Mur.	CAGCCATCCCATCCACCCAGGTCGTCCTATTCTTCTTTGAGGAGACAGCCAGCGAGTTTGACTTCTTTGA						
	770	780	790	800	810	820	830

Fig. 27K

Fig. 27L

1090	1100	1110	1120	1130	1140	1150
Hum.	GGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCC					
	CC					
	CC					
Mur.	GGGAAGTACAAGGAGCTGAACAAGGAGACCTCCCCGCTGGACCACCTTACCGGGGCTCAGAGGTCAGCCCCGA					
1120	1130	1140	1150	1160	1170	1180
1160	1170	1180	1190	1200	1210	1220
Hum.	GGCCAGGCAGTTGCTCAGTGGGCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCCTGAT					
	CC					
	CC					
Mur.	GGCCAGGCAGTTGCTCAGTGGGCCCTCCTCTGACAAAGCCTTGACCTTCATGAAGGACCATTTTCTGAT					
1190	1200	1210	1220	1230	1240	1250
1230	1240	1250	1260	1270	1280	1290
Hum.	GGATGAGCAAGTGGTGGGACGCCCTGCTGGTGAATCTGGCGTGGAGTATACACGGCTTGCAAGTGGAG					
	CC					
	CC					
Mur.	GGATGAGCACGTGGTAGGAACACCCCTGCTGGTGAAGTCTGGTGTGGAGTACACACGGCTTGCTGTGGAG					
1260	1270	1280	1290	1300	1310	1320
1300	1310	1320	1330	1340	1350	1360
Hum.	ACAGCCCAGGGCCCTTGATGGGCACAGCCCATCTTGTCATGTACCTGGAAACCAACACAGGGTCGCTCCACA					
	CC					
	CC					
Mur.	TCAGCTCGGGGCCCTTGATGGGAGCAGCCCATGTGGTCATGTATCTGGGTACCTCCACGGGTCCCCCTGCACA					
1330	1340	1350	1360	1370	1380	1390

Fig. 27M

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1370      1380      1390      1400      1410      1420      1430
Hum.  AGGCTGTGTAAGTGGGACAGCAGTGCTCATCTGGTGAAGAGATTTCAGCTGTTCCCTGACCCTGAACC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  AGGCTGTGTCCTCAGGACAGCAGTGCTTATCTCGTGGAGGAGATTTCAGCTGAGCCCTGACTCTGAGCC
1400      1410      1420      1430      1440      1450      1460

1440      1450      1460      1470      1480      1490      1500
Hum.  TGTTTCGCAACCTGCAGCTGGCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGCTGGAGG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  TGTTTCGAAACCTGCAGCTGGCCCCCGCCAGGGTGCAGTGTTTGCAGGCTTCTCTGGAGGCATCTGGAGA
1470      1480      1490      1500      1510      1520      1530

1510      1520      1530      1540      1550      1560      1570
Hum.  GTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGCCCCGGGACCCCACTGTG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  GTTCCCAGGGCCAAATTGCAGTGTCTACGAGAGCTGTGTGGACTGTGTGCTTGCCAGGACCCCTCACTGTG
1540      1550      1560      1570      1580      1590      1600

1580      1590      1600      1610      1620      1630      1640
Hum.  CCTGGGACCCCTGAGTCCCGAACCTGTTGCCCTCCTGTCTGCCCCCAACCTGAACCTCCTGGAAGCAGGACAT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  CCTGGGACCCCTGAATCAAGACTCTGCAGCCTTCTGTCTGGCTC-TACCAAGCCT--TGGAAAGCAGGACAT
1610      1620      1630      1640      1650      1660      1670

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Fig. 27N

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1650      1660      1670      1680      1690      1700      1710
Hum.  GGAGCGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  GGAACGCGGCAACCCGGAGTGGGTATGCACCCGTGGCCCCCATGGCCAGGAGCCCCCGGCTCAGAGCCCC
1680      1690      1700      1710      1720      1730      1740

1720      1730      1740      1750      1760      1770      1780
Hum.  CCGCAAAATCATTAAGAGTCCTGGCTGTCCCAACTCCATCCTGGAGCTCCCTGCCCCACCTGTCTCAG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  CCTCAACTAATTAAGAGTCCTGACAGTCCCAACTCCATCCTGGAGCTGCGCTGCCCCACCTGTCTCAG
1750      1760      1770      1780      1790      1800      1810

1790      1800      1810      1820      1830      1840      1850
Hum.  CCTTGGCCCTCTATTATTGGAGTCATGGCCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAAATGG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  CACTGGCCCTCTTACCACTGGAGTCATGGCCGAGCCAAAATCTCAGAAGCCTCTGTACCGTCTACAAATGG
1820      1830      1840      1850      1860      1870      1880

1860      1870      1880      1890      1900      1910      1920
Hum.  CTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGTCTCTACCACTGTGGGCAACTGAGAATGGCTTT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  CTCCCTCTTGCTGCTGCCGAGGATGGTGTCTGGGGCCCTCTACCACTGTGTGGCGACTGAGAACGGCTAC
1890      1900      1910      1920      1930      1940      1950

```

Fig. 270

	1930	1940	1950	1960	1970	1980	1990
Hum.	TCATACCCCTGTGATCTCCTACTGGTGGACAGCCAGACCCCTGGCCCTGGATCCTGAACCTGGCAG						
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
Mur.	TCATACCCCTGTGGTCTCCTATTGGGTAGACAGCCAGACCCCTGGCGCTGGACCCCTGAGCTGGCGG						
	1960	1970	1980	1990	2000	2010	2020
	2000	2010	2020	2030	2040	2050	2060
Hum.	GCATCCCCCGGAGCATGTGAAGGTCCCCTTGACCAGGGTCAGTGGTGGGCGCGCCCTGGCTGCCCAGCA						
	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::
Mur.	GCGTCCCCCGTGAGCGTGTGCAGGTCCCGCTGACCAGGGTCGGAGCGGAGCTTCCATGGCTGCCCAGCG						
	2030	2040	2050	2060	2070	2080	2090
	2070	2080	2090	2100	2110	2120	2130
Hum.	GTCCTACTGGCCCCACTTTGTCACTGTCACTGTCTCTTTGCCCTTAGTGCTTTCAGGAGCCCTCATCATC						
	::::::::::	:::: ::::	:::: ::::	:::: ::::	:::: ::::	:::: ::::	:::: ::::
Mur.	GTCCTACTGGCCCCCATTTTCTCATCGTTACCGTCCCTCCTGGCCATCGTGCTCCTGGAGTGCTCACTCTC						
	2100	2110	2120	2130	2140	2150	2160
	2140	2150	2160	2170	2180	2190	2200
Hum.	CTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGCAAGGTCAGGGCTGTGAGACCCCTGCGCCCTG						
	::: : ::	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::	::: ::::
Mur.	CTCCTCGCTTCCCCACTGGGGCGGCTCGGGGTAAGGTCAGGGCTGTGGGATGCTGCCCCCA						
	2170	2180	2190	2200	2210	2220	2230

Fig. 27P

	2210	2220	2230	2240	2250	2260	2270
Hum.	GGGAGAGGCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGA						

Mur.	GGGAAAAGGCTCCACTGAGCAGGACCAAGCACCTCCAGCCCTCCAAGGACCAAGGACCTCTGCCAGTGA						
	2240	2250	2260	2270	2280	2290	2300
	2280	2290	2300	2310	2320	2330	2340
Hum.	TGTGGACGCTGACAAACAAGTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGG-CGGGGGCTG--C						

Mur.	CGTAGATGCCGACAAACAACCATCTGGCGCCGAAGTGGCTTAAACA-GGGACACAGATCCGCAGCTGAGC						
	2310	2320	2330	2340	2350	2360	2370
	2350	2360	2370	2380	2390	2400	2410
Hum.	GGTGAGGCACCTGGCCATGCTGGCTGGCGGCCCAAGCACAGCCCCTGACTAGGATGACAGCAGCACAAA						

Mur.	AGAGCAAGCCACTGGCCCTTGTGGCTATGC-----CAGGCACAG-----TGCCACTCT--						
	2380	2390	2400	2410			2420
	2420	2430	2440	2450	2460	2470	2480
Hum.	AGACCACCTTTCTCCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGC						

Mur.	-GACCA-----GGGTAGGAG--GCT-CT-C-CTGCTA-ACGTGTGTTCAC-CTACAG-----C						
		2430	2440	2450	2460		

Fig. 27Q

	2490	2500	2510	2520	2530	2540	2550
Hum.	ACAGCAGTCTG-CCTCCCTATGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGCT						
	:: :::: : :::::::::::::: ::::: ::::: :::::						:::::
Mur.	ACC-CAGTAGGTCCCTCCCTGTGGACTCTCTTCTGC-AAGCACATT-----GGGCT						
	2470	2480	2490	2500	2510		
	2560	2570	2580	2590	2600	2610	
Hum.	ACCCCAGACCTGCTCCTACACTGATA-TTGAAGAACCCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAG						
	. : :::: : . : :::: : . : ::::::::::: ::::: ::::: ::::: ::::: .. ::::						
Mur.	GTCGCCATACCTGTACTTGCTGTGACAGGAAGAGCCAGAC-AGGTTCTTTGATTTTGATTGACCCAA						
	2520	2530	2540	2550	2560	2570	2580
	2620	2630	2640	2650	2660	2670	2680
Hum.	GGACCCCT-CCAGAAACACA-GTGTTTCAAGAGATCCTAAAAAACCCTGCCTGTCCAGACCCCTATGGTA						
	: ::::: ::::::::::: : ::::: : ::::::::::: : ::::: ::::: ::::: ::::: :::::						
Mur.	GAGCCCTGCCCTGTAAACAAACGTGCTCCAGGAGA-CCATGAAAAGGTGTGGCTGTCT-GGGATTCTGTGGTG						
	2590	2600	2610	2620	2630	2640	2650
	2690	2700	2710	2720	2730	2740	2750
Hum.	ATGAACACCAAACATCTAAACAATCATATGCTAA-CATGC---CAC--TCCTGGAAACT-CCACTCTGAA						
	: :::: : ::::::::::: ::::: : . : ::::: : ::::: : ::::: : ::::: : ::::: : ::::: :						
Mur.	ACAAAC-CTAAGCATCCGAGCAAGCTGGGGCTATTCTTGCAAACTCCATCCTGAACGCTGTCACTCTAGA						
	2660	2670	2680	2690	2700	2710	2720

Fig. 27R

```

2760      2770      2780      2790      2800      2810
Hum.  ----GCTGCCGCTTTGGACACCAACACTCCCTTCT-CCCAGG-GTCATGCAGGGATCTGCTCCCTCCTGC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  AGCAGCTGCTGCTTTGAACACACAGCCACCCCTCCTTCCCAAGAGTCTCTATGGAGTTGGC-CCCTTGTGT
2730      2740      2750      2760      2770      2780      2790

2820      2830      2840      2850      2860      2870      2880
Hum.  TTCCCTTACCAGTCGTGCACCCGCTGACTCCAGGAAGTCTTCTGAAGTCTGACCACTTCTTCTTGTG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  TTCCCTTACCAGTCGGGCCATACCTGTTT---GGGAAGTCATCTCTGAAGTCTAACCACTTCTTCTTGG
2800      2810      2820      2830      2840      2850

2890      2900      2910      2920      2930      2940      2950
Hum.  TTCAGTTGGGCAGACTCTGATCCCT---TCTGCCCTGGCAGAAATGGCAGGGGTAATCTGAGCCTTCTTC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  TTCAGTTTGGACAGATTGTTATTATTGTCTCTGCCCTGGCTAGAAATGGGGGCATAATCTGAGCCTTGTTC
2860      2870      2880      2890      2900      2910      2920

2960      2970      2980      2990      3000      3010
Hum.  ACTCCCTTTACCC---TAGCTGACCCCTTACCTCTCCC--CCTCCCTTTTCTTGTTTGGGATTCAGA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  ---CCTTGTCAGTGTGGCTGACCC-TTGACCTCTTCCCTTCCCTCC---TCCCTTTGTTTGGGATTCAGA
2930      2940      2950      2960      2970      2980      2990

```

Fig. 27S

```

3020      3030      3040      3050      3060      3070      3080
Hum.  AAAC TGCTGTCAGAGACTGTTATTTTATTTAAATAATAAGGCTTAAAAAATAAAAAA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  AAAC TGCTGTCAGAGACAATTTATTTTATTTTATTTAAATA-----AGATATAA
      3000      3010      3020      3030

3090      3100
Hum.  AAAAAAAGGCGGCCGC
      . . . . .
Mur.  GCTTTAAAG-----
      3040

```

Fig. 27T

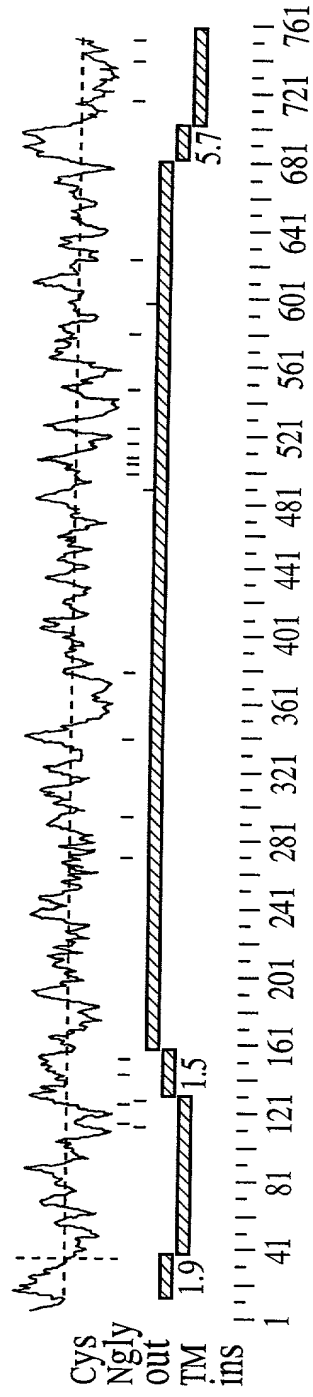


Fig. 27U

GTGACCCACGGTCCGCAGCTTTGGACACTTCCTCTGCTTGAGGACACCTTGACTAACCTCCAAGGGCAACTAAAGGA	79
TCAAGAAAGGCCAGCACAGCAGAAGATCAGCTGGATCTAGCTCCTGCAGGAG ATG TGT ACA AAG ACA ATC	150
	6
P V L W G C F L L L W N L Y V S S S Q T I	26
CCA GTC CTC TGG GGA TGT TTC CTC CTC TAT GTC TCA TCC TCT CAG ACC ATT	210
Y P G I K A R I T Q R A L D Y G V Q A G	46
TAC CCT GGA ATC AAG GCA AGG ATT ACT CAG AGG GCA CTT GAC TAT GGT GGT CAA GCT GGA	270
M K M I E Q M L L K E K K K L P D L S G S E	66
ATG AAG ATG ATT GAG CAA ATG CTA AAA GAA AAG AAA CTC CCA GAT TTA AGC GGT TCT GAG	330
S L E F L K V D Y V N Y N F S N I K I S	86
TCT CTT GAA TTT CTA AAA GTT GAT TAT GTA AAC TAC AAT TTT TCA AAT ATA AAA ATC AGT	390
A F S F P N T S L A F V P G V G I K A L	106
GCC TTT TCA TTT CCA AAT ACC TCA TTG GCT TTT GTG CCT GGA GTG GGA ATC AAA GCG CTA	450
T N H G T A N I S T D W G F E S P L F V	126
ACC AAC CAT GGC ACT GCC AAC ATC AGC ACA GAC TGG GGG TTC GAG TCT CCA CTT TTT GTT	510
L Y N S F A E P M E K P I L K N L N E M	146
CTG TAT AAC TCC TTT GCT GAG CCC ATG GAG AAA CCC ATT TTA AAG AAC TTA AAT GAA ATG	570

Fig. 28A

L C P I I A S E V K A L N A N L S T L E 166
 CTC TGT CCC ATT ATT GCA AGT GAA GTC AAA GCG CTA AAT GCC AAC CTC AGC ACA CTG GAG 630

 V L T K I D N Y T L L L D Y S L I S S P E 186
 GTT TTA ACC AAG ATT GAC AAC TAC ACT CTG CTG GAT TAC TCC CTA ATC AGT TCT CCA GAA 690

 I T E N Y L D L N L K G V F Y P L E N L 206
 ATT ACT GAG AAC TAC CTT GAC CTG AAC TTG AAG GGT GTA TTC TAC CCA CTG GAA AAC CTC 750

 T D P P F S P V P F V L P E R S N S M L 226
 ACC GAC CCC CCC TTC TCA CCA CCA GTT CCT TTT GTG CTC CCA GAA CGC AGC AAC TCC ATG CTC 810

 Y I G I A E Y F F K S A S F A H F T A G 246
 TAC ATT GGA ATC GCC GAG TAT TTC TTT AAA TCT GCG TCC TTT GCT CAT TTC ACA GCT GGG 870

 V F N L T L S T E I S N H F V Q N S Q 266
 GTT TTC AAT CTC ACT CTC TCC ACC GAA GAG ATT TCC AAC CAT TTT GTT CAA AAC TCT CAA 930

 G L G N V L S R I A E I Y I L S Q P F M 286
 GGC CTT GGC AAC GTG CTC TCC CGG ATT GCA GAG ATC TAC ATC TTG TCC CAG CCC TTC ATG 990

 V R I M A T E P P I I N L Q P G N F T L 306
 GTG AGG ATC ATG GCC ACA GAG CCT CCC ATA ATC ATC AAT CTA CAA CCA GGC AAT TTC ACC CTG 1050

 D I P A S I M L T Q P K N S T V E T I 326
 GAC ATC CCT GCC TCC ATC ATG ATG CTC ACC CAA CCC AAG AAC TCC ACA GTT GAA ACC ATC 1110

Fig. 28B

Figure 28C

V	S	M	D	F	V	A	S	T	S	V	G	L	V	I	L	G	Q	R	L	346
GTT	TCC	ATG	GAC	TTC	GTT	GCT	AGT	ACC	AGT	GTT	GGC	CTG	GTT	ATT	TTG	GGA	CAA	AGA	CTG	1170
V	C	S	L	S	L	N	R	F	R	L	A	L	P	E	S	N	R	S	N	366
GTC	TGC	TCC	TTG	TCT	CTG	AAC	AGA	TTC	CGC	CTT	GCT	TTG	CCA	GAG	TCC	AAT	CGC	AGC	AAC	1230
I	E	V	L	R	F	E	N	I	L	S	S	I	L	H	F	G	V	L	P	386
ATT	GAG	GTC	TTG	AGG	TTT	GAA	AAT	ATT	CTA	TCG	TCC	ATT	CTT	CAC	TTT	GGA	GTC	CTC	CCA	1290
L	A	N	A	K	L	Q	Q	G	F	P	L	P	N	P	H	K	F	L	F	406
CTG	GCC	AAT	GCA	AAA	TTG	CAG	CAA	GGA	TTT	CCT	CTG	CCC	AAT	CCA	CAC	AAA	TTC	TTA	TTC	1350
V	N	S	D	I	E	V	L	E	G	F	L	L	I	S	T	D	L	K	Y	426
GTC	AAT	TCA	GAT	ATT	GAA	GTT	CTT	GAG	GGT	TTC	CTT	TTG	ATT	TCC	ACC	GAC	CTG	AAG	TAT	1410
E	T	S	S	K	Q	Q	P	S	F	H	V	W	E	G	L	N	L	I	S	446
GAA	ACA	TCC	TCA	AAG	CAG	CAG	CCA	AGT	TTC	CAC	GTA	TGG	GAA	GGT	CTG	AAC	CTG	ATA	AGC	1470
R	Q	W	R	G	K	S	A	P	*											456
AGA	CAG	TGG	AGG	GGG	AAG	TCA	GCC	CCT	TGA											1500
TTGCCGGTTT	GCAATT	CACCC	CAGGA	GTAAAT	GGTCCT	TAACT	CTACAACT	ACTGTAA	ACCCAGAA	GGAAAGACAGT	1579									
ACACACT	GGAATT	GTAAAG	CCCTT	GTGAA	TTGCTT	AGGCAGAA	AGTTT	CTTCTT	CTTAAGCCTT	CAGGAACCCAGAAATAA	1658									
GGCAGACT	CTGTTAA	AGGGATA	AAATAG	AGGTG	CTGAAT	GTGAGT	GTATGCAT	GCTGCCGT	GCTGTGTTAT	GTTTG	1737									
TTTGTTT	GTTGGG	CAAGAA	GATTCT	AGGACAA	GAGCTAG	GCATGTACTT	CTGACCAGGT	GGGTAAGCA	ACTCTAAG	1816										

Fig. 28C

TCTGTATTGGTCATTCTCAGTGGAAATCCCTTAGGCCCTCTAGTGGTTTTCCTACCTGCATATTGGTTTC 1895
ATGTTTATATTCACCTGTTACTATCTTCTGTGTTTAAATTGTTTCTATCAAAAAAAAAAAAAAAAAAGGGC 1974
GGCCGC 1980

Fig. 28D

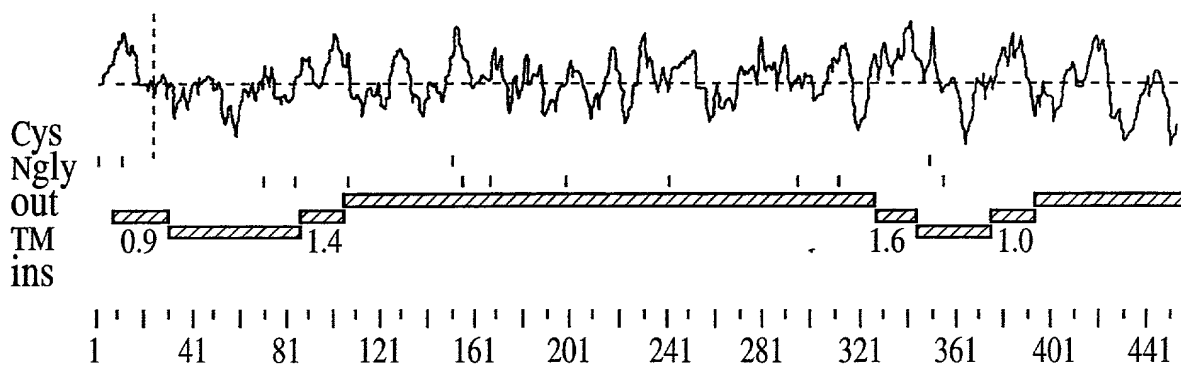


Fig. 28E

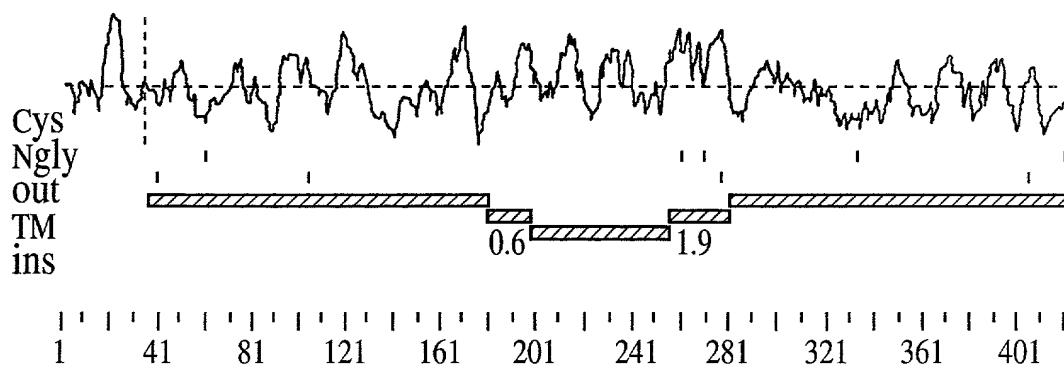


Fig. 29F

```

10      20      30      40      50      60
286 MCTKT-IPVLWGCFL-LWNLVSSSQTIYPGIKARITQRALDYGVAQGMKMIQMLKEKLPDLGSESL
      :      :      :      :      :      :      :      :      :      :
BPI MARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS--DSF
      10      20      30      40      50      60

      70      80      90      100     110     120     130
286 EFLKVDYVYNFNSNIKISAFSPNTSLAFVPGVGIGIKALTNHGTANISTDWGFESPLFVLYNSFAEPME--
      .      .      .      :      :      :      :      :      :      :
BPI KIKHLGKGHYSFYSMDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFLKMSGNFDLSIEGM
      70      80      90      100     110     120     130

286 -----KPI-----140      150
      :      :
BPI SISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKSKVGWLIQLFHKKIESALRNKMNSQVCEKVTNS
      140     150     160     170     180     190     200

      160     170     180     190     200     210     220
286 VKA-LNANLSTLEVLTKIDNYTLDDYSLISSPEITENYLDLNLKGVFYPLENLTDPPFSPVPFVLPERSN
      :      :      :      :      :      :      :      :      :      :
BPI VSSKLQPYFQTLPVMTKIDSVAGINYGVLVAPPATTAETLDVQMKGEFYSENHHNPPPPFAPPVMEFPAAMD
      210     220     230     240     250     260     270

```

Fig. 28F

230	240	250	260	270	280	290
286	SMLYIGIAEYFFKSA	FAHFTAGVFNLT	STEEISNH--FVQNS	QGLGNVLSRIA	EIYILSQPFMVR	IMA
BPI	RMVYLG	SDYFFNTAGLV	YQEA	GLKMTL	RDDMIPKESK	FRLLTTKFFG
280	290	300	310	320	330	340
286	TEPPIIN	LQPGNFTL	DIPASIMMLT	QPKNSTVETIV	SMDFVASTV	GLVILGQRLV
BPI	STPPHLS	VQPTGLTF	YPADVQAF	AVLPNSSLAS	LFLIGMHTT	GSMEVSAESN
350	360	370	380	390	400	410
286	SNRSNIEV	LRFFENIL	SSILHFGV	LPANAKLQ	QGFFLPNPHK	FLFVN
BPI	SNIGFP	VELLQD	IMNYIV	PILVLP	RVNEKLQ	KGFFLPTPAR
420	430	440	450	460	470	480
286	QQPSFH	VWEGNL	LISRQW	RKSAP		
BPI	-----					

Figure 28H

```

10      20      30      40      50      60
286 MCTKTIPVLWGCFLWNLYVSSSQTI--YPGIKARITQRALDYGVDQAGMKMIEQMLKEKKLPDLSGSESL
: . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RENP MGALARAL--PSILLALLTSTPEALGANPGLVARITDKGLQYAAQEGLLALQSELLRITLPDFTG--DL
10      20      30      40      50      60

70      80      90      100     110     120     130
286 EFLKVDYVNYNFSNIKISAFSPNTSLAFVPGVGIGKALTNHGTANISTDWGFESPLFVLYNSFAEPME--
: . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RENP RIPHVGRGRYEFHSLNIHEFQLPSSQISMVPNVGLKFSISNANIKISGKWKAKRFLKMSGNFDLSIEGM
70      80      90      100     110     120     130

286 -----KPI-----140     150
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RENP SISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKSKVGWLIQLFHKKIESALRNKMNSQVCEKVTNS
140     150     160     170     180     190     200

160     170     180     190     200     210     220
286 VKA-LNANLSTLEVLTKIDNYTLDDYSLISSPEITENYLDNLKGVFYPLENLTDPFSPVPFVLPERSN
: . : . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RENP VSSKLQPYFQTLPVMTKIDSVAGINYGVLVAPPATTAEITLDVQMKGEFYSENHHNPPPPFAPPVMEFPAHD
210     220     230     240     250     260     270

```

Fig. 28H

Fig. 281

GTCGACCCACGCGTCCGGGGAATTGCAGCAGGAAATAATGTGAAGAGTTTTTAAACCCACAAAATCTTCTTACTTTAGA 79

ATTAGTTGTACATTGGCAGGAAAAATAAATGCAGATGTTGGACC ATG TTG GAA ACC TTG TCA AGA CAG 8

W I V S H R M E M W L L I L V A Y M F Q 28

TGG ATT GTC TCA CAC AGA ATG GAA ATG TGG CTT CTG ATT CTG GTG GCG TAT ATG TTC CAG 209

R N V N S V H M P T K A V D P E A F M N 48

AGA AAT GTG AAT TCA GTA CAT ATG CCA ACT AAA GCT GTG GAC CCA GAA GCA TTC ATG AAT 269

I S E I I Q H Q G Y P C E E Y E V A T E 68

ATT AGT GAA ATC ATC CAA CAT CAA GGC TAT CCC TGT GAG GAA TAT GAA GTC GCA ACT GAA 329

D G Y I L S V N R I P R G L V Q P K K T 88

GAT GGG TAT ATC CTT TCT TCT GTT AAC AGG ATT CCT CGA GGC CTA GTG CAA CCT AAG AAG ACA 389

G S R P V V L L Q H G L V G G A S N W I 108

GGT TCC AGG CCT GTG GTG TTA CTG CAG CAT GGC CTA GTT GGA GGT GCT AGC AAC TGG ATT 449

S N L P N N S L G F I L A D A G F D V W 128

TCC AAC CTG CCC AAC AAT AGC CTG GGC TTC ATT CTG GCA GAT GCT GGT TTT GAC GTG TGG 509

M G N S R G N A W S R K H K T L S I D Q 148

ATG GGG AAC AGC AGG GGA AAC GCC TGG TCT CGA AAA CAC AAG ACA CTC TCC ATA GAC CAA 569

Fig. 29A

D	E	F	W	A	F	S	Y	D	E	M	A	R	F	D	L	P	A	V	I	168
GAT	GAG	TTC	TGG	GCT	TTC	AGT	TAT	GAT	GAG	ATG	GCT	AGG	TTT	GAC	CTT	CCT	GCA	GTG	ATA	629
N	F	I	L	Q	K	T	G	Q	E	K	I	Y	Y	V	G	Y	S	Q	G	188
AAC	TTT	ATT	TTG	CAG	AAA	ACG	GGC	CAG	GAA	AAG	ATC	TAT	TAT	GTC	GGC	TAT	TCA	CAG	GGC	689
T	T	M	G	F	I	A	F	S	T	M	P	E	L	A	Q	K	I	K	M	208
ACC	ACC	ATG	GGC	TTT	ATT	GCA	TTT	TCC	ACC	ATG	CCA	GAG	CTG	GCT	CAG	AAA	ATC	AAA	ATG	749
Y	F	A	L	A	P	I	A	T	V	K	H	A	K	S	P	G	T	K	F	228
TAT	TTT	GCT	TTA	GCA	CCC	ATA	GCC	ACT	GTT	AAG	CAT	GCA	AAA	AGC	CCC	GGG	ACC	AAA	TTT	809
L	L	L	P	D	M	M	I	K	G	L	F	G	K	K	E	F	L	Y	Q	248
TTG	TTG	CTG	CCA	GAT	ATG	ATG	ATC	AAG	GGA	TTG	TTT	GGC	AAA	AAA	GAA	TTT	CTG	TAT	CAG	869
T	R	F	L	R	Q	L	V	I	Y	L	C	G	Q	V	I	L	D	Q	I	268
ACC	AGA	TTT	CTC	AGA	CAA	CTT	GTT	ATT	TAC	CTT	TGT	GGC	CAG	GTG	ATT	CTT	GAT	CAG	ATT	929
C	S	N	I	M	L	L	L	G	G	F	N	T	N	N	M	N	M	S	R	288
TGT	AGT	AAT	ATC	ATG	TTA	CTT	CTG	GGT	GGA	TTC	AAC	ACC	AAC	AAT	ATG	AAC	ATG	AGC	CGA	989
A	S	V	Y	A	A	H	T	L	A	G	T	S	V	Q	N	I	L	H	W	308
GCA	AGT	GTA	TAT	GCT	GCC	CAC	ACT	CTT	GCT	GGA	ACA	TCT	GTG	CAA	AAT	ATT	CTA	CAC	TGG	1049
S	Q	A	V	N	S	G	E	L	R	A	F	D	W	G	S	E	T	K	N	328
AGC	CAG	GCA	GTG	AAT	TCT	GGT	GAA	CTC	CGG	GCA	TTT	GAC	TGG	GGG	AGT	GAG	ACC	AAA	AAT	1109

Fig. 29B

L E K C N Q CAG CCA ACT CCT GTA AGG TAC AGA GTC AGA GAT ATG ACG GTC CCT P 348
 CTG GAA AAA TGC AAT CAG CCA ACT CCT GTA AGG TAC AGA GTC AGA GAT ATG ACG GTC CCT 1169

 T A M W T G G Q D W L S N P E D V K M L 368
 ACA GCA ATG TGG ACA GGA GGT CAG GAC TGG CTT TCA AAT CCA GAA GAC GTG AAA ATG CTG 1229

 L S E V T N L I Y H K N I P E W A H V D 388
 CTC TCT GAG GTG ACC AAC CTC ATC TAC CAT AAG AAT ATT CCT GAA TGG GCT CAC GTG GAT 1289

 F I W G L D A P H R M Y N E I I H L M Q 408
 TTC ATC TGG GGT TTG GAT GCT CCT CAC CGT ATG TAC AAT GAA ATC ATC CAT CTG ATG CAG 1349

 Q E E T N L S Q G R C E A V L * 424
 CAG GAG GAG ACC AAC CTT TCC CAG GGA CGG TGT GAG GCC GTA TTG TGA 1397

 AGCATCTGACACTGACGATCTTAGGACAACCTCCTGAGGGATGGGGCTAGGACCCATGAAGGCAGAAATTACGGAGAGCA 1476
 GAGACCTAGTATACATTTTTCAGATTCCTGCACTTGGCAGTAAATCCGACACTTACATTTTCTGTAAA 1555
 TTTAAAGTACTTATTAGGTAAATAGAGGTTTGTATGCTATTATATATTCTACCATCTTGAAGGGTAGGTTTACCTGAT 1634
 AGCCAGAAAATATCTAGACATTTCTATATCATTCAGGTAATCTCTTTAAACACCTATTGTTTTCTCTATAAGCCAT 1713
 ATTTTGGAGCCTAAAGTAAATGGCAAAATGGGACAGATAATTGAGGCTCTGGAGTCTGTGATATTGTTGACTTTGA 1792
 CAAAATAAGCTAGACATTTTCACCTTGTGCCCACAGAGACATAACACTACCTCAGGAAGCTGAGCTGCTTTAAGGACAA 1871
 CAACAACAAAATCAGTGTTACAGTATGGATGAAATCTATGTTAAGCATTTCTCAGATAAGGCCAAGTTTATAGTTGCA 1950
 TCTCAGGGGAAAGAAAATTTTATAGGATGTTTATGAGTCTCTCCAATAAATGCATTCTGCATTACATAAAAAA 2029
 AAAAAGGGGCGCGC 2044

Fig. 29C

```

10      20      30      40      50      60      70
294 MLETLRQWIVSHRMEMWLLILVAYMFQRNVNSVHMPKAVDPEAFMNISEIIHQHGYPCEEYEVATEDG
:   ...   :   :   :   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
HLP M-----WLL---LTMASLISVLGTTGHLFGKLH-----PGSPEVTMNIISQMITYWGYPNEEYEVVTEDEG
10      20      30      40      50

80      90      100     110     120     130     140
294 YILSVNRIPRGLVQPKKKTGSRPVVLLQHGLVGGASNWISNLPNNSLGFILADAGFDVWMGNSRGNWSRK
:   :   :   :   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
HLP YILEVNRIPYGKKNSGNTGQRPVVFLQHGLLASATNWNISNLPNNSLAFILADAGYDVWLGNRGNTWARR
60      70      80      90      100     110     120

150     160     170     180     190     200     210
294 HKTLSIDQDEFWAFSYDEMAREFDLPVAVINFILQKTGQEKIYYVGYSGQTTMGFIAFSTMPPELAQIKMYF
.   :   :   :   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
HLP NLYYSPDSVEFWAFSFDDEMAKYDLPATIDFIVKKTGQKQLHYVGHSGQTTIGFIAFSTNPSLAKRIKTFY
130     140     150     160     170     180     190

220     230     240     250     260     270
294 ALAPIATVKHAKSPGTKFLLLPDMMIKGLFGKKEFLYQTRFLRQ-LVIYLCGQVILDDQICSNIMLLLGFF
:   :   :   :   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
HLP ALAPVATVKYTKSLINKLRFVPQSLFKFIFGDKIF-YPHNFFDQFLATEVCSREMLNLLCSNALFIICGF
200     210     220     230     240     250     260

```

Fig. 29D


```

10      20      30      40      50      60
294 MLETLRQWIVSHRMEMWLLILVAYMFQRNVNSVHMPTK--AVDPEAFMNISEIIHQHGYPCPEEYEVATE
:      :...: . . . . :      :      :      :      :      :      :      :
LAL M-----KMRFLGLVVCLVLWPLHSEGGKLTAVDPETNMNVSEIISYWGFPSSEYLVETE
      10      20      30      40      50

70      80      90      100     110     120     130
294 DGYILSVNRIPRGLVQPKKTGSRPVVLLQHGLVGASNWISNLPNNSLGFILADAGFDVWMGNSRGNWS
:      :      : .      :      :      :      :      :      :      :
LAL DGYILCLNRI PHGRKNHSDKGPVVF LQHGLLADSSNWVTNLANS LGFILADAGFDVWMGNSRGNTWS
      60      70      80      90      100     110     120

140     150     160     170     180     190     200
294 RKHKTLSDQDEFWAFSYDEMAREFDLPVINFILQKTGQEKIYYVGYSQGTMTMGFIASFSTMPELAQIKM
:      :      :      :      :      :      :      :      :      :      :
LAL RKHKTLVSQDEFWAFSYDEMAYDLPASINFILNKTGQEQVYVVGHSQGTIGFIASFQIPELAKRIKM
      130     140     150     160     170     180     190

210     220     230     240     250     260     270
294 YFALAPIATVKHAKSPGTFLLLPDMMIKGLFGKKEFLYQTRFLRQLVIYLCGQVILDQICSNIMLLGG
:      :      : . . . . :      :      :      :      :      :      :
LAL FFALGPVASVAFCTSPMAKLGRLPDHLIKDLFGDKFELPQSAFLKWLGHVCTHVILKELCGNLCFLLCG
      200     210     220     230     240     250     260

```

Fig. 29G

Fig. 29C

```
280      290      300      310      320      330      340
294 FNTNNMMSRASVYAAHTLAGTSVQNIILHWSQAVNSGELRAFDWGSETKNLEKCNQPTPVRVVRDMTVP
   :: :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
LAL FNERNLNMSRVDVYTTHTSPAGTSVQNNMLHWSQAVKFKQAFDWSGSAKNYFHYNQSYPPTYNVKDMMLVP
270      280      290      300      310      320      330

350      360      370      380      390      400      410
294 TAMWTGGQDWLSNPEDVKMLLSEVTNLIYHKNIPEWAHVDFIWGLDAPHRMYNEIIHLMQQEETNLSQGR
   :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
LAL TAVWSGGHDWLADVVDVNILLTQITNLVFHESIPWEHLDFIWGLDAPWRLYNKIINLMRKYQ-----
340      350      360      370      380      390

420
294 CEAVL

LAL -----
```

Fig. 29H

																M S		2		
GTCGACCCACGCGTCCACGGAGGGCTCCCGGGCGCAGCATTTGCCCCCTGCACCACCTCACCAAG ATG GCT																		75		
T L G H T F P F Y A G P K P T F P M D T																			22	
ACT TTG GGA CAC ACA TTC CCC TTC TAT GCT GGC CCC AAG CCA ACC TTC CCG ATG GAC ACC																			135	
T L A S I I M I F L T A L A T F I V I L																			42	
ACT TTG GCC AGC ATC ATC ATG ATC TTT CTG ACT GCA CTG GCC ACG TTC ATC GTC ATC CTG																			195	
P G I R G K T R L F W L L R V V T S L F																			62	
CCT GGC ATT CGG GGA AAG ACG AGG CTG TTC TGG CTG CTT CGG GTG GTG ACC AGC TTA TTC																			255	
I G A A I L A V N F S S E W S V G Q V S																			82	
ATC GGG GCT GCA ATC CTG GCT GCT GTG AAT TTC AGT TCT GAG TGG TCT GTG GGC CAG GTC AGC																			315	
T N T S Y K A F S S E W I S A D I G L Q																			102	
ACC AAC ACA TCA TAC AAG GCC TTC AGT TCT GAG TGG ATC AGC GCT GAT ATT GGG CTG CAG																			375	
V G L G G V N I T L T G T P V Q Q L N E																			122	
GTC GGG CTG GGT GGA GTC AAC ATC ACA CTC ACA GGG ACC CCC GTG CAG CAG CTG AAT GAG																			435	
T I N Y N E E F T W R L G E N Y A E E C																			142	
ACC ATC AAT TAC AAC GAG GAG TTC ACC TGG CGC CTG GGT GAG AAC TAT GCT GAG GAG TGT																			495	
A K A L E K G L P D P V L Y L A E K F T																			162	
GCA AAG GCT CTG GAG AAG GGG CTG CCA GAC CCT GTG TTG TAC CTA GCT GAG AAG TTC ACT																			555	

Fig. 30A

P	R	S	P	C	G	L	Y	R	Q	Y	R	L	A	G	H	Y	T	S	A	182
CCA	AGA	AGC	CCA	TGT	GGC	CTA	TAC	CGC	CAG	TAC	CGC	CTG	GCG	GGA	CAC	TAC	ACC	TCA	GCC	615
M	L	W	V	A	F	L	C	W	L	L	A	N	V	M	L	S	M	P	V	202
ATG	CTA	TGG	GTG	GCA	TTC	CTC	TGC	TGG	CTG	CTG	GCC	AAT	GTG	ATG	CTC	TCC	ATG	CCT	GTG	675
L	V	Y	G	G	Y	M	L	L	A	T	G	I	F	Q	L	L	A	L	L	222
CTG	GTA	TAT	GGT	GGC	TAC	ATG	CTA	TTG	GCC	ACG	GGC	ATC	TTC	CAG	CTG	TTG	GCT	CTG	CTC	735
F	F	S	M	A	T	S	L	T	S	P	C	P	L	H	L	G	A	S	V	242
TTC	TTC	TCC	ATG	GCC	ACA	TCA	CTC	ACC	TCA	CCC	TGT	CCC	CTG	CAC	CTG	GGC	GCT	TCT	GTG	795
L	H	T	H	H	G	P	A	F	W	I	T	L	T	T	G	L	L	C	V	262
CTG	CAT	ACT	CAC	CAT	GGG	CCT	GCC	TTC	TGG	ATC	ACA	TTG	ACC	ACA	GGA	CTG	CTG	TGT	GTG	855
L	L	G	L	A	M	A	V	A	H	R	M	Q	P	H	R	L	K	A	F	282
CTG	CTG	GGC	CTG	GCT	ATG	GCG	GTG	GCC	CAC	AGG	ATG	CAG	CCT	CAC	AGG	CTG	AAG	GCT	TTC	915
F	N	Q	S	V	D	E	D	P	M	L	E	W	S	P	E	E	G	G	L	302
TTC	AAC	CAG	AGT	GTG	GAT	GAA	GAC	CCC	ATG	CTG	GAG	TGG	AGT	CCT	GAG	GAA	GGT	GGA	CTC	975
L	S	P	R	Y	R	S	M	A	D	S	P	K	S	Q	D	I	P	L	S	322
CTG	AGC	CCC	CGC	TAC	CGG	TCC	ATG	GCT	GAC	AGT	CCC	AAG	TCC	CAG	GAC	ATT	CCC	CTG	TCA	1035
E	A	S	S	T	K	A	Y	C	K	E	A	H	P	K	D	P	D	C	A	342
GAG	GCT	TCC	TCC	ACC	AAG	GCA	TAC	TGT	AAG	GAG	GCA	CAC	CCC	AAA	GAT	CCT	GAT	TGT	GCT	1095

Fig. 30B

L * 344
TTA TAA 1101

CATTCTCCCGTGGAGGCCACCTGGACTTCAGTCTGGCTCCAAACCTCAATTGGCGCCCATATAAACCCAGCAGAACTG 1180
CCCTCAGGGTGGCTGTACCAGACACCCAGCACCAATCTACAGACGGAGTAGAAAAAGGAGGCTCTATATACTGATGTT 1259
AAAAAACAAAAACAAAAAGCCCTAAGGACTGAAGAGATGCTGGGCTGTCCATAAAGCCGTGTGCCATGATAAG 1338
GCCAAGCAGGGCTAGCTTATCTGCACAGCAACCCAGCCCTTCCGTGCTGCCCTTGCCTCTTCAAGATGCTATTCACCTGA 1417
AACCTAACTTCACCCCATAAACACAGCAGGGTGGGGTTACATATGATTCTCCCTATGGTTTCCCTCTCATCCCTCGGCA 1496
CCTCTGTTTTCCTTTTCTGGGTTCCCTTTTGTCTTCTTACTTCTCCAGCTTGTGTGGCCTTTTGGTACAATGAA 1575
AGACAGCACTGGAAAGGAGGGGAAACCAAACCTTCTCATCTAGGTCTAACATTAAACCACTATGCCACATTCCTCTTGA 1654
GCTTCAGTCCCAAATTTGCTACATAAGATTGCAAGACTTGCCAAAGATCTTGGGATTATCTTCTATGCTTGGCTGA 1733
CACCTACCTTGGCCCTCAAACACACCACTCACAAAGCCAGGTGGGAAGTTAGGGAATCAACTCCAAAACGCTATTCCT 1812
TCCACCCCACTCAGCTGGCTAGCTGAGTGGCATCCAGGACGGGGAGTGGGTGACCTGCCCTCATCACTGCCACCTAA 1891
CGTCCCCCTGGGTGGTTCAGAAAGATGCTAGCTCTGGTAGGTCCTCCGGCCTCACTAGAGGCGCCCTATTACTC 1970
TGGAGTCGACGCAGAGAAATCAGGTTTCACAGCACTGCCGAGAGTGTACTAGGCTGTCTCCAGCCAGCGAAAGCTCATGA 2049
GGACGTGCGACCCCGCGGAGAGCCATGAAAATTAATGGGAAAAAACAGTTTAAAAAAGGCGG 2128
GCGGC 2133

Fig. 30C

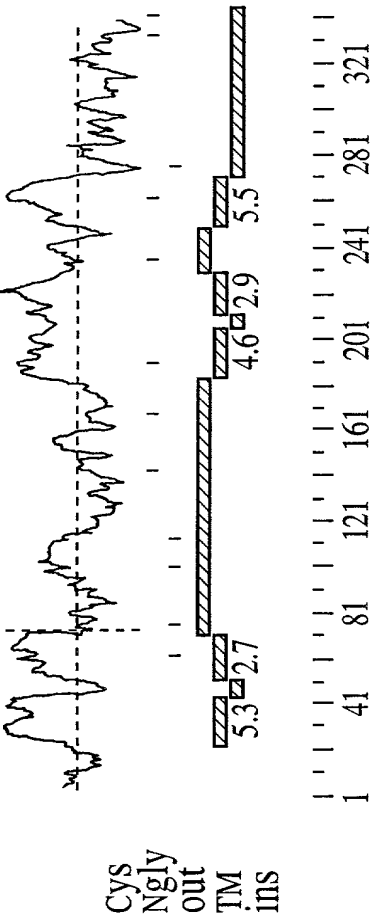


Fig. 300

```

10      20      30      40      50      60      70
296 MATLGHTFPFYAGPKPTFPMDTTLASIIMIFLTALATFIVILPGIRGKTRLFWLLRVVTSLSFIGAAILAV
: .. :... .. :... .. :... .. :... .. :... .. :... .. :... ..
CRP M-RIAH-----ASSRGNI-----SIFSFLIPLIAYILILPGVR-RKRVVTTVTYVLMMLAVGGALIAS
10      20      30      40      50
296 NFSSEWSVGQVSTNTSYKAFSSEWISADIGLQVGLGGVNITL-----TGTPVQQQLNETIN--YNEEFTW
. . . : :... :... :... :... :... :... :... :... :... :
CRP LIYPCWASGSQMIYTQFRGHSNERILAKIGVEIGLQKVNVTLLKFERLLSSNDVLPGSDMTELYYNEGFDI
60      70      80      90      100      110      120      130

```

Fig. 30E

```

140      150      160      170      180      190      200
296 RLGENYAECAKALEKGLPDPVLYLAEKFT-PRSPCGLYRQYRLAGHYTSAMLWVAFLCWLLANV-MLISM
CRP  . : : . : : : : : : : : : : : : : : : : : : : : : : : : : : :
130      140      150      160      170      180      190
SGISSMAEALHHGLENGLPYPMLSVLEYFSLNQDSFDWGRHYRVAGHYTHAAIWFAFACWCISVVLMFL

210      220      230      240      250      260
296 PVLVYGGYMLLATGIFQLLALLFFSMATSLTSPCPLHL---GASVLHTHHGPAF---WITLTGLLCVL
CRP  : : . : : : : : : : : : : : : : : : : : : : : : : : : : : :
200      210      220      230      240      250      260
PHNAYKS--ILATGISCLIACLVYL---LLSPCELRIAFGTGENFERVDLTATFSFCFYLIFAIGILCVL

```

Fig. 30F

Cell "Cell"

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270      280      290      300      310      320
296 LGLAMAVAHRMQPHRLKAFNQSVDEDPMLEW-----SPEEGLLSPRY--RSMADSPKSQDIPLSEAS
CRP  CGGLGIGICEHWRIYTLSTFLDASLDEHVGPWKKLPTGGPALQGVQIGAYGTNTTNSSRDKNDISSDKTA
      270      280      290      300      310      320      330
      330
296 STKAY-----CK-----EAHPKDPD-----CA---L
CRP  GSSGFQSRSTSTCQSSASSASLRSQSSIETVHDEAELEERTHVHFLQEPCCSSST
      340      350      360      370      380

```

Fig. 30G